

```

TTGGCCTGAC CATCTTTGTG CTGTCTGTCG TCACTATCAT CATCTGCTTC ACCTGCTCCT 180
GCTGCTGCCT TTACAAGACG TGCCGCCGAC CACGTCCGGT TGTACCACC ACCACATCCA 240
CCACTGTGGT GC ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT 291
      Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala
      -15                      -10                      -5

ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG 339
Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln
      1                      5                      10

GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT ACC CAC CAC CTT ACC CAG 387
Gly Cys Gln Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln
      15                      20                      25                      30

CCC AGC CCA TGG GCC CAC CGG SCT ACC ACG AGA CCC TGG CTG GAG GAG 435
Pro Ser Pro Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu
      35                      40                      45

CAG CCG CGC CCC GGG 450
Gln Pro Arg Pro Gly
      50

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 85..139
id AA157672
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 86..140
id AA157671
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..94

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
 region 10..47
 id HUML116
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..263
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
 seq LRRLGCLTLTSL/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATTGCGTAG TTCCGAATAC CCTCGGCCAC ACCTGGCCTT CTCC ATG CTC GGA ATA	56
Met Leu Gly Ile	
-70	
ACT TCC TGC AGC GAC CAA CAG GCT AAA GAG GGG GAA GGT CTG GAG GGA	104
Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu Gly Leu Glu Gly	
-65 -60 -55	
TCC AGC ACC GGC TCC TCC TCC GGC AAC CAC GGT GGG AGC GGC GGA GGA	152
Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly	
-50 -45 -40	
AAT GGA CAT AAA CCC GGG TGT GAA AAG CCA GGG AAT GAA GCC CGC GGG	200
Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly	
-35 -30 -25	
AGC GGG AAT CTG GGA TTC AGA ACT CTG AGA CGT CTC CTG GGA TGT TTA	248
Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu Leu Gly Cys Leu	
-20 -15 -10	
ACT TTG ACA CTT TCT GGA AGA ATT	272
Thr Leu Thr Leu Ser Gly Arg Ile	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..137
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91

region 190..271
id AA103102
. est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..108
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 143..191
id AA103102
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 72..122
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq ALKLASWTSMLA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
AAATCCCCG CTACGGGGT GCGGCCGGAA GCCGGGCGCC GCGGCTCTGC TTCCTCGGG 60
GATCTGGCGA C ATG GCC AGA AAG GCT CTC AAG CTT GCT TCG TGG ACC AGC 110
      Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser
                -15                -10                -5

ATG GCT CTT GCT GCC TCT GGC ATC TAC TTC TAC AGT AAC AAG TAC TTG 158
Met Ala Leu Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu
                1                5                10

GAC CCT AAT GAC TTT GGC GCT GTC AGG GTG GGC AGA GCA GTT GCT ACG 206
Asp Pro Asn Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr
                15                20                25

ACG GCT GTC ATC AGT KAC GAC TAC CTC ACT TCC CTG AAC AGT GTC CCT 254
Thr Ala Val Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro
                30                35                40

TAT GGC TCA GAG GAG TAC TTG CAG CTG AGA TCT AAG GTG CAC CTT CGC 302
Tyr Gly Ser Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg
                45                50                55                60

TCT GCC AGG CGT CTC TGT NAR STC TGC TGT GCC AAC CGG GGC 344
Ser Ala Arg Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
                65                70
```

(2) INFORMATION FOR SEQ ID NO: 196:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 13..406
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..394
 id AA284513
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 18..343
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 7..332
 id H99096
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 363..403
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 355..395
 id H99096
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 13..371
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..359
 id AA020823
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 27..406
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 17..396
 id N21197
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 24..290
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 11..277
 id AA083141
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 10..57

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6

.seq AALPAWLSLQSR/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

CTCGCAGCC ATG GCG GCC GCC GCG CTC CCA GCA TGG CTG TCT CTG CAG TCG    51
      Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser
          -15                      -10                      -5

AGG GCA AGG TCT CTG CGT GCA TTC TCC ACT GCC GTC TAC TCG GCC ACT    99
Arg Ala Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr
      1                      5                      10

CCG GTC CCG ACA CCT AGC CTG CCG GAA AGA ACA CCC GGA AAT GAA AGG    147
Pro Val Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg
      15                      20                      25                      30

CCA CCA AGN AGA AAG GCA CTA CCT CCT AGG ACA GAG AAA ATG GCT GTT    195
Pro Pro Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val
          35                      40                      45

GAC CAG GAC TGG CCT AGT GTT TAC CCA GTT GCA GCA CCA TTB AAA CCC    243
Asp Gln Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro
          50                      55                      60

TCT GCA GTA CCT CTT CCT GTT CGA ATG GGT TAT CCA GTA AAA AAG GGC    291
Ser Ala Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly
          65                      70                      75

GTG CCC ATG GCA AAG GAG GGA AAT CTA GAA CTT TTA AAG ATT CCC AAT    339
Val Pro Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn
          80                      85                      90

TTT CTG CAT TTG ACT CCT GTA GCA ATT AAA AAG CAC TGT GNR GCC CTT    387
Phe Leu His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu
          95                      100                      105                      110

AAA GAT TTT TGC ACT GAG
Lys Asp Phe Cys Thr Glu
          115

```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 92..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 83..446
id W37917
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 5..85
id W37917
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..446
id AA010474
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..84
id AA010474
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 79..289
id W77834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 363..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 345..432
id W77834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..106
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 6..80
id W77834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 288..349
id W77834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 85..374
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 3..74
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 389..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 370..436
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 183..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 153..430
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..66
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 114..164
id AA169869

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 104..144
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 77..117
 id AA169869
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 118..312
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq CMLTLXXLSFILA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

GTAGTGT TAG ACTGAAGATA AAGTAAGTGC TGTTTGGGCT AACAGGATCT CCTCTTGCAG      60
TCTGCAGCCC AGGACGCTGA TTCCAGCAGC GCCTTACCGC GCASCCGAAG ATTCACT      117
ATG GTG AAA ATC GCC TTC AAT ACC CCT ACC GCC GTG CAA AAG GAG GAG      165
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65                      -60                      -55                      -50
GCG CGG CAA GAC GTG GAG GCC CTC CTG AGC CGC ACG GTC AGA ACT CAG      213
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
-45                      -40                      -35
ATA CTG ACC GGC AAG GAG CTC CGA GTT GCC ACC CAG GAA AAA GAG GGC      261
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
-30                      -25                      -20
TCC TCT GGG AGA TGT ATG CTT ACT CTC TTN NVC CTT TCA TTC ATC TTC      309
Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
-15                      -10                      -5
GCA GGA CTT ATT GTT GGT GGA GCC TGC ATT TAC AAG TAC TTC ATG CCC      357
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
1                      5                      10                      15
AAG AGC ACC ATT TAC CGT GGA NAG ATG TGC TTT TTT GAT TCT GAG GAT      405
Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
20                      25                      30
CCT GCA AAT TCC CTT CGT GGA GGA GAG CCT AAC TTC CTG CCT GTG ACT      453
Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 198:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Thyroid

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..161
id HUM085F04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..109
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..101
id AA143653
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(62..155)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 24..117
id H17554
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..185
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 139..221
id H18908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 109..185
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 133..209
id H25714
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 11..154
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LLLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

AAACCGCGCC ATG ATA GGG TCG GGA TTG GCT GGC TCT GGA GGC GCA GGT      49
      Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly
                -45                      -40

GGT CCT TCT TCT ACT GTC ACA TGG TGC GCG CTG WTT TCT AAT CAC GTG      97
Gly Pro Ser Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val
-35                -30                      -25                      -20

GCT GCC ACC CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG      145
Ala Ala Thr Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
                -15                      -10                      -5

CTG CTG CCT GAT GGC CTC CCG CCW TTT GTT GCT ACC CCG ATG      187
Leu Leu Pro Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
                1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 202..319
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 316..406
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 167..284
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 281..364
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..137
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..296
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 213..292
id W25483

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..182
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 307..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 177..294
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 329..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 288..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 313..366
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LXGFLEFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```
AATAACTGAA AGTAGCTAAG GCACCCAGC CGGAGGAAGT GAGCTCTCCT GGGGCGTGGT   60
TGTTTCGTGAT CCTTGCATCT GTTACTTAGG GTCAAGGCTT GGGTCTTGCC CCGCAGACCC   120
TTGGGACGAC CCGGCCCCAG CGCASTATGA ACCTGGAGCG AGTGTCCAAT GAGGAGAAAT   180
TGAACCTGTG CCGGAAGTAC TACCTGGGGG GGTTCGCTTT CCTGCCTTTT CTCTGGTTGG   240
TCAACATCTT CTGGTTCTTC CGAGAGGCCT TCCTTGTCCT AGCCTACACA GAACAGAGCC   300
AAATCAAAGG CT ATG TCT GGC GCT CAG CTK HTG GGC TTC CTC TTC TGS GTG   351
      Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val
              -15                      -10

ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC CGC   399
Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg
-5              1              5              10

TGG GGG TGC CCT TGG GGA CTA CCT CTC CTT CAC ATA CCC CTG GGC ACC   447
Trp Gly Cys Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr
      15              20              25

CCT GAC AAC TTC TGC ACA TAC   468
Pro Asp Asn Phe Cys Thr Tyr
      30
```

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 328..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 15..119
id HUMGS01778
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: complement(256..309)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 175..228
id HSAAAAJHX
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 188..274
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq VVFMTVAASGASS/FA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```
ACGGTTCCGG GCGTTACCAT CGTCCGTGCG CACCGCCCGG CGTCCAGGTG AGTCTCCCAT   60
CTGCAGAGAC GCGGACGCGC CGGCCCGCAG TTGGCCTGCG GACGCGGTGG ACGGTTTGGC   120
GCCCACCAGG CGATCAATAC TTTGGATTTT TAATTTCTAG ATTGGCAAT TCTTCGCTGA   180
AGTCATC ATG AGC TTT TTC CAA CTC CTG ATG AAA AGG AAG GAA CTC ATT   229
    Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile
                    -25                               -20

CCC TTG GTG GTG TTC ATG ACT GTG GCG GCG AGT GGA GCC TCA TCT TTC   277
Pro Leu Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe
-15                    -10                               -5                               1

GCT GTG TAT TCT CTT TGG AAA ACC GAT GTG ATC CTT GAT CGA AAA AAA   325
Ala Val Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys
                    5                               10                               15

AAT CCA GAA CCT TGG GAA ACT GTG GAC CCT ACT GTA CCT CAA AAG CTT   373
Asn Pro Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu
                20                    25                    30

ATA ACA ATC AAC CAA CAA TGG AAA CCC ATT GAA GAG TTG CAA AAT GTC   421
Ile Thr Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val
                35                    40                    45

CAA AGG GTA ACG   433
Gln Arg Val Thr
50
```

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..242)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..215
id N91097
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 103..147
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

GCGGGAGSTG GGGCATCCGG GTCTCTTGGT GGCTGCTTCT ACCCCCGGAG CTCAGCTGAT   60
CTTCCCTTCC AGACTACGAG GTGTGAATTT CAAACTTCCG TA ATG GAG TTA GCC   114
                               Met Glu Leu Ala
                               -15

CAC AGT TTA TTG CTA AAT GAA GAA GCT TTG GCT CAA ATC ACC GAA GCA   162
His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln Ile Thr Glu Ala
-10                               -5                               1                               5

AAA AGA CCA GTT TTC ATC TTT GAA TGG TTG CGA TTT CTT GAT AAA GTC   210
Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe Leu Asp Lys Val
                               10                               15                               20

TTG GTT GCT GCC AAC AAG ACC GAT GTA AAG GAA AAA CAG AAA AAA CTT   258
Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys Gln Lys Lys Leu
                               25                               30                               35

GTT GAA CAA TTA ACT GGA TTA ATA AGT AGT TCA CCT GGA CCC ACC GGG   306
Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro Gly Pro Thr Gly
                               40                               45                               50

```

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 6..322
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 15..331
 id H23844
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 11..322
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 21..332
 id H22656
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 12..310
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 8..306
 id AA036876
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 22..204
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..183
 id W05714
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 205..305
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 183..233
 id W05714
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 40..322

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..283
id R69117
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..139
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```
CTGAAGCCGG AAGCTACCTA TCTGGTAGGG AGCTCCCCCA GCACCGAAGA CTGCG ATG      58
                                         Met
ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC CAG CTC GGC      106
Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu Gly
   -25                      -20                      -15

TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT GGG GAC CTG      154
Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp Leu
   -10                      -5                      1                      5

GAG AAT GAT GAG CAG GCA GCC AGT GCC ATC TCT GAG CTG GTC AGC ACA      202
Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser Thr
               10                      15                      20

GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC TTC AAG CGC      250
Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys Arg
               25                      30                      35

CTG TCT GTG GTC TTT GGA GAA CAC ACA CTG CTG GTG ACG GTG TCA GGA      298
Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser Gly
               40                      45                      50

CAG AGG GTG TTT GTG GTG AAG AAG GGG      325
Gln Arg Val Phe Val Val Lys Arg Gly
               55                      60
```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..374
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 125..358
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..119
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 388..452
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 374..438
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 131..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 113..315
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..137
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 43..120
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 323..374
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 304..355
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 338..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 371..416
id AA143062
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..317
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 388..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 370..416
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 8..46
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..359
id HUM159G08B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..47
id HUM159G08B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..316
id N34957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 30..97
id N34957

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 12..104
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq LVGVLFVSVTTG/PW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

AGGTCCTCAA G ATG GCG GCC GCC TGG CCG TCT GGT CCG KCT GCT CCG GAG      50
      Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
            -30                -25                -20

GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC TCA GTC ACT      98
Ala Val Thr      Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
            -15                -10                -5

ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC GAG GAG TCG      146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
            1                5                10

CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT AAA GAT CCA      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
            15                20                25                30

AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA AAC TAC ACA      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
            35                40                45

GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT AAG GAT NCC      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa
            50                55                60

AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT TTT TTC AAG      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
            65                70                75

CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC NNT KAG CAG TNN      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa
            80                85                90

NWT GTC TCT TTT TCT TGG ATG GTT GGG AGC AGA TCG ATT TTA CCT TGG      434
Xaa Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
            95                100                105                110

ATA CCC TSC TTT GGG TTT GTT      455
Ile Pro Cys Phe Gly Phe Val
            115

```

(2) INFORMATION FOR SEQ ID NO: 204:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 170..201

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 157..188
id AA102919
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 117..155

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

AAGCAGCTGG ATCTCCGGTA ACTGAGACAT AGGGTATAAC TGTTGTCGCG GCGGAGGAAG 60

TGAGGACGGC GCCAAGGGCC TTCCGGGCCA GTGTTGGATC CCTGTAGTTT GTGAAG ATG 119
Met

GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG GAC GGG CTC CCG CTG GCC 167
Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu Ala
-10 -5 1

GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC CGG 200
Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
5 10 15

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 121..436

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 57..372

id AA023107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 157..399
id AA102919
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 141..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```
AACCTCAGCG GGAAGCGGAG ACGCAAGCAG CTKGATCTCC GGTAACTGAG ACATAGGGTA   60
TAACTGTGTG CGCGGCGGAG GAAGTGAGGA CGGCGCCAAG GGCCTTCCGG GGCAGTGTG   120
GATCCCTGTA GTTTGTGAAG ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG   173
      Met Val Leu Leu Thr Met Ile Ala Arg Val Ala
                        -10                        -5

GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC   221
Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly
      1                      5                      10

CGG GAC GTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA AAG   269
Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys
     15                      20                      25                      30

TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC ATG   317
Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met
                        35                      40                      45

ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA TGT   365
Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys
                        50                      55                      60

GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT TTG   413
Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu
      65                      70                      75

CAC TCA GAA TTT GAT GAA CAG   434
His Ser Glu Phe Asp Glu Gln
     80                      85
```

(x) INFORMATION FOR SEQ ID NO: 206:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 86..333
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 7..81
id AA035203
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 349..378
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..288
id R97144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..94
id R97144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 63..353
id H64963

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 38..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..58
id H64963
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..392
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 32..322
id W03796
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 86..340
id N73170
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 3..81
id N73170
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 117..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq MMVLSLGIXLASA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
AAGAAGATGA AGGTAAGTAG AAACCGTTGA TGGGACTGAG AAACCAGAGT TAAACCTCT   60
TTGGAGCTTC TGAGGACTCA GCTGGAACCA AMCGGGCACA GTTTGGCAAC ACCATC ATG   119
                                         Met
ACA TCA CAA CCT GTT CCC AAT GAG ACC ATC ATA GTG CTC CCA TCA AAT   167
Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser Asn
      -65                      -60                      -55

CTC ATC AAC TTC TCC CAA GCA GAG AAA CCC GAA CCC ACC AAC CAG GGG   215
Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly
      -50                      -45                      -40
```

```

CAG GAT AGC CTG AAG AAA CAT CTA CAC GCA GAA ATC AAA GTT ATT GGG      263
Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile Gly
  -35                      -30                      -25

ACT ATC CAG ATC TTG TGT GGC ATG ATG GTA TTG AGC TTG GGG ATC AKT      311
Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile Xaa
 -20                      -15                      -10                      -5

TTG GCA TCT GCT TCC TTC TCT CCA AAT TTT ACC CAA GTG ACT TCT ACA      359
Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser Thr
                      1                      5                      10

CTG TTG AAC TCT GCT TAC CCA TTC ATA GGA CCC TTT TTT TTT ATC ATC      407
Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile
      15                      20                      25

TCT GGC TCT CTA TCA ATC                                          425
Ser Gly Ser Leu Ser Ile
      30

```

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..347
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 369..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 346..393
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 379..412
id W81335

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..240
id W03593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 239..347
id W03593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 233..389
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..177
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 162..310
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 325..406
id W81261
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..273
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..233
id AA151036
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..430
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 232..389
id AA151036
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..112
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

ATTTTTTTTT CGAGACCGGA AGTGAGTGAT CGAAAGC ATG GCG TCG GTG GTG TTG	55
Met Ala Ser Val Val Leu	
-25 -20	
GCG CTG AGG ACC CGG ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG	103
Ala Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro	
-15 -10 -5	
GCT ACA GCT CTT GCT GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC	151
Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser	
1 5 10	
TCC AAA AAC CTC GGT GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG	199
Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys	
15 20 25	
AAA ATG GAA GGT CAC TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG	247
Lys Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln	
30 35 40 45	
CGC CAT TTC CGC TGG CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG VNT	295
Arg His Phe Arg Trp His Pro Gly Ala His Val Gly Val Gly Lys Xaa	
50 55 60	
AAA TGT CTG TAT GCC CTG GAA GAG GGG ATA GTC CGC TAC ACT AAG GAG	343
Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu	
65 70 75	
GTC TAC GTG CCT CAT CCC AGA AAC ACG GAG GCT GTG GRT CTG ATC ACC	391

Val Tyr Val Pro His Pro Arg Asn Thr Glu Ala Val Xaa Leu Ile Thr
80 85 90

AGG CTG HYC AAG GGT GCT GTG CTC TAC AAG ACT TTT GTC ACG TGG TTC 439
Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys Thr Phe Val Thr Trp Phe
95 100 105

CTG 442
Leu
110

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..347
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 381..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 376..421
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 352..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 346..383
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..224
id AA156841

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 257..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 233..402
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..233
id AA151036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 232..402
id AA151036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..413
id W69555
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..177
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 162..310
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 325..419
id W81261
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..95
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

GGAAGTGAGT GATCGAAAGC ATG GCG TCG GTG GTG TTG GCG CTG AGG ACC CGG      53
      Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg
      -25                      -20          -15

ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG GCT ACA GCT CTT GCT      101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
      -10                      -5              1

GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC TCC AAA AAC CTC GGT      149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
      5                      10              15

GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG AAA ATG GAA GGT CAC      197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
      20                      25              30

TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG CGC CAT TTC CGC TGG      245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp
      35                      40              45              50

CAC CCA GGT GGC CAT GTG GGT GTT GGG AAG AAT AAA TGT CTG TAT GCC      293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala
      55                      60              65

CTG GAA GAG GGG ATA VWC CGC TAC ACT AAG GAG CTC TAC GTG CCT CAT      341
Leu Glu Glu Gly Ile Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His
      70                      75              80

CCC AGA AAC ACA GAG GCT GTG GAT CTG ATC ACC AGG CTG CCC AAG GGT      389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly
      85                      90              95

GCT GTG CTC TAC AAG ACT TTT GTC CAC GTG GTT CCT      425
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro
      100                      105              110

```

(x) INFORMATION FOR SEQ ID NO: 209:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 89..321
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..391
id W68063
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68063
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..50
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68063
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 78..313
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 15..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 364..393
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..378
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 62..313
id AA083574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 296..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 312..345
id AA083574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 97..320
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 3..90
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 333..390
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 86..321
id R70112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..94
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 40..87
id R70112
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 111..281
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AIALATVLFLLGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```
ATGAGTGGCA CTTAAGCGGG CCATGCCATG CAACCTTGGG CGCTGCCAAC CGTGGGCGAG   60
CTCTGGGTGT GCGGGCGGCC TGGCGCGGCG CTCCGCTGTG TCAGCGTGT ATG ATG   116
                                         Met Met
CCG TCC CGT ACC AAC CTG GCT ACT GGA ATC CCC AGT AGT AAA GTG AAA   164
Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys Val Lys
-55                               -50               -45               -40
TAT TCA AGG CTC TCC AGC ACA GAC GAT GGC TAC ATT GAC CTT CAG TTT   212
Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu Gln Phe
-35                               -30               -25
AAG AAA ACC CCT CCT AAG ATC CCT TAT AAG GCC ATC GCA CTT GCC ACT   260
Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu Ala Thr
-20                               -15               -10
GTG CTG TTT TTG ATT GGC GCC TTT CTC ATT ATT ATA GGC TCC CTC CTG   308
Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser Leu Leu
-5                               1               5
CTG TCA GGC TAC ATC AGC AAA GGG GGG GCA GAC CGG GCC GTT CCA GTG   356
Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val Pro Val
10                               15               20               25
CTG ATC ATT GGC ATT CTG GTG TTC CTA CCC GGA TTT TAC CAC           398
Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
30                               35
```

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 19..351
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 12..344
 id W22200
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 22..351
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..330
 id R87595
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 111..287
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 110..286
 id R88526
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 1..112
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..112
 id R88526
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 118..331
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 96..309
 id AA031849
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 23..112
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 49..289
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..53
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 242..286
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
GAAAATTGAA ACTGAGTGGC CCACGATGGG AAGASGGGAA AGCCCAGGGG TACAGGAGGC   60
CTCTGGGTGA AGGCAGAGGC TAACATGAGG TTCGGAGCGA CCTTGGCCGT TGGCCTGACC  120
ATCTTTGTGC TGTCTGTGCT CACTATCATC ATCTGCTTCA CCTGCTCCTG CTGCTGCCTT  180
TACAAGACGT GCCGCCGACC ACGTCCGGTT GTCACCACCA CCACATCCAC CACTGTGGTG  240
C ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT ACC CTG GAC   289
Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15                -10                -5                1

CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG GGA TGC CAG   337
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
5                10                15

CAG CAC CCT ACN NAC CAG
Gln His Pro Thr Xaa Gln   355
20
```

(2) INFORMATION FOR SEQ ID NO: 211:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 49..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 12..358
id W22200
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 52..383

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..332
id R87595
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..317

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 110..286
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 31..142

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..112
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 148..361

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 96..309
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 58..142

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 141..395
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 49..303
 id T08643
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 93..144
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 2..53
 id T08643
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 272..316
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

AGATTGCTT TCTTTTCTC CAAAAGGGA GGAAATTGAA ACTGAGTGSC CCACGATGGG   60
AAGAGGGGAA AGCCCAGGGG TACAGGAGGC CTCTGGGTGA AGGCAGAGGC TAACATGGGG   120
TTCGGAGCGA CCTTGGCCGT TGGCCTGACC ATCTTTGTGC TGTCTGTCGT CACTATCATC   180
ATCTGCTTCA CCTGCTCCTG CTGCTGCCTT TACAAGACGT GCCGCCGACC ACGTCCGGTT   240
GTCACCACCA CCACATCCAC CACTGTGGTG C ATG CCC CTT ATC CTC AGC CTC   292
                               Met Pro Leu Ile Leu Ser Leu
                               -15                      -10

CAA GTG TGC CGC CCA GCT ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA   340
Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
                               -5                      1                      5

CCA TGC CGC CTC AGC CAG GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT   388
Pro Cys Arg Leu Ser Gln Gly Cys Gln Gln His Pro Thr Gln Cys Ser
                               10                      15                      20

ACC CAC CTT GGG
Thr His Leu Gly
                               25

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 152..420
id AA146275
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 152..420
id AA146400
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 199..402

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ATTTTTC AAG ACCGTACTAG GTAGATGGTC AATTAGAGTT CCCAGGGTTT GAAGCCTGTA 60

ACTGCTGCCG CCGCTCAAGC CCTCCAGAGC ATTGCTACGG CTGCTGCCCT TGTACTACTA 120

CCTCCAAATA CGTTCTTGCT GGTAGTGGCG GCAGCAGGAC CAATTACCTC TTTTGTGCTC 180

TCCCTCGAGA AGCTCCAG ATG GCG TCT TCC GTG GGC AAC GTG GCC GAC AGC 231
Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser
-65 -60

ACA GAA CCA ACG AAA CGT ATG CTT TCC TTC CAA GGG TTA GCT GAG TTG 279
Thr Glu Pro Thr Lys Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu
-55 -50 -45

GCA CAT CGA GAA TAT CAG GCA GGA GAT TTT GAG GCA GCB GAG AGA CAC 327
Ala His Arg Glu Tyr Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His
-40 -35 -30

TGC ATG CAG CTC TGG AGA CAA GAG CCA GAC AAT ACT GGT GTG CTT TTA 375
Cys Met Gln Leu Trp Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu
-25 -20 -15 -10

TTA CTT TCA TCT ATA CAC TTC CAG TGT CGA AGG CTG GAC AGA TCT GCT 423
Leu Leu Ser Ser Ile His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala
-5 1 5

CAC TTT AGC ACT CTG GCA
His Phe Ser Thr Leu Ala
10

441

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..218
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 268..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 248..359
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..65
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..47
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 43..228
id AA134712
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..379
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 225..361
id AA134712
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..65
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..47
id AA134712
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 48..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq VILQLQFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

ATTGATAGG CGCCGGGCAG CTGAGCTGGT AGGAGGACCA GACGGGG ATG TTC GGC	56
Met Phe Gly	
TCC GCC CCC CAG CGT CCC GTG GCC ATG ACG ACC GCT CAG AGG GAC TCC	104
Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln Arg Asp Ser	
-90 -85 -80	
CTG TTG TGG AAG CTC GCG GGG TTG CTG CGG GAG TYY GGG GAT GTG GTC	152
Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly Asp Val Val	
-75 -70 -65 -60	
CTG TCT GGC TGT AGC ACC CTG AGC CTG CTG ACT CCC ACA CTG CAA CAG	200
Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr Leu Gln Gln	
-55 -50 -45	
CTG AAC CAC GTA TTT GAG CTG CAC CTG GGG CCA TGG GGC CCT GGC CAG	248
Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly Pro Gly Gln	
-40 -35 -30	
ACA GGC TTT GTG GCT CTG CCC TCC CAT CCT GCC GAC TCC CCT GTT ATT	296
Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser Pro Val Ile	
-25 -20 -15	
CTT CAG CTT CAG TTT CTC TTC GAT GTG CTG CAG AAA ACA CTT TCA CTC	344
Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr Leu Ser Leu	
-10 -5 1 5	
AAG CTG GTC CAT GTT GCT GGT CCT GGC CCC ACA	377
Lys Leu Val His Val Ala Gly Pro Gly Pro Thr	
10 15	

(2) INFORMATION FOR SEQ ID NO: 214:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 80..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 61..312
id N23581
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..77
id N23581
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 328..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 310..369
id N23581
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 119..292
id AA088606
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 328..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 290..349
id AA088606
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..156
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 62..118

id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 13..64
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..331)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 234..518
id HSGT511
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..387)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 177..236
id HSGT511
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 73..314
id W89716
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 314..371
id W89716
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 118..350
id W42358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 350..407
id W42358
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..377
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq LILVGTSKHVAFG/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

AGTACATCCG GCGAGTAGCT GGCGGTCCCG GGTGCTGCTG GTTAGTGTGC TGTGAGGGAG   60
GGTCCGAGCC AGCCGCTGTT TTGCCGAGAG AGCCCTCAG GCGTAGTAA GCATTAATA   119
ATG TCT TTC ATC TTT GAG TGG ATC TAC AAT GGC TTC AGC AGT GTG CTC   167
Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu
-85                               -80                               -75
CAG TTC CTA GGA CTG TAC AAG AAA TCT GGA AAA CTT GTA TTC TTA GGT   215
Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly
-70                               -65                               -60                               -55
TTG GAT AAT GCA GGC AAA ACC ACT CTT CTT CAC ATG CTC AAA GAT GAC   263
Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
-50                               -45                               -40
AGA TTG GGC CAA CAT GTT CCA ACA CTA CAT CCG ACA TCA GAA GAG CTA   311
Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
-35                               -30                               -25
ACA ATT GCT GGA ATG ACC TTA CAA CTT TTG ATC TTG GTS GGC ACG AGC   359
Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser
-20                               -15                               -10
AAG CAC GTC GCG TTT GGA AAA ATT ATC
Lys His Val Ala Phe Gly Lys Ile Ile
-5                               1

```

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 74..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 78..183
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 176..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 181..266
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..74
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 4..77
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 262..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 263..297
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 54..297
id W44615
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..61
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..34
id W44615
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..267
id W69940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 57..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..199
id W16769
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 255..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 198..264
id W16769
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..199
id N46069
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..290
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..253
id N46069
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 196..300
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq WYSTVGLLPPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
AAAGACGCTC ACGGGCGCGC GGAATATCGG GCGGCTAGGC TCTCTGAGGA GGCTGCCACA 60
GTGAAGCAAC CGTGACAAGT GGTGCCCCGAC CAGGGACCTG AACGAGGAAG GTCTGCCAGA 120
GCAGAGAAAG TGAAACTGAT CAGACGAACT ACGAACCCCT GGACGGGAGA GTCTGCCGGC 180
GGAGAATATA AGGAG ATG GAC AAA CCG TGT GGG TGC CCT CCA GGT GTG TGT 231
      Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys
      -35             -30             -25

GAC CAT GGA ACG GGA GAC CGG AGG GAT CCA TGG TAT TCA ACC GTG GGC 279
Asp His Gly Thr Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly
      -20             -15             -10

CTG TTA CCT CCA GTA CGA GCC ATG AGC CAG CGG AAT CTG AAT 321
```

Leu Leu Pro Pro Val Arg Ala Met Ser Gln Arg Asn Leu Asn
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 161..327
id H07981
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..211
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..155
id H07981
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 193..355
id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 88..188
id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 9..33

id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 163..369
id H19239
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 59..164
id H19239
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 2..51
id H19239
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..178
id AA096397
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 337..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 296..330
id AA096397
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..266
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 203..232
id AA096397
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 212..345
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 145..278
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 59..121
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 68..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..57
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 25..132
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq ARALAALVPGVTQ/VD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

AGTTTCCGGT TCGCCTCCGG AGCC ATG GCG GCG GCA CTG AAG TGT CTA CTG	51
Met Ala Ala Ala Leu Lys Cys Leu Leu	
-35 -30	
ACA TTA GGA AGA TGG TGC CCC GGC CTT GGA GTG GCT CCC CAG GCC CGG	99
Thr Leu Gly Arg Trp Cys Pro Gly Leu Gly Val Ala Pro Gln Ala Arg	
-25 -20 -15	
GCG CTC GGC GGC TTA GTA CCC GGA GTG ACC CAG GTA GAT AAC AAG TCC	147
Ala Leu Ala Ala Leu Val Pro Gly Val Thr Gln Val Asp Asn Lys Ser	
-10 -5 1 5	
GGT TTC CTG CAG AAG AGG CCT CAT CGC CAG CAC CCT GGC ATC CTA AAG	195
Gly Phe Leu Gln Lys Arg Pro His Arg Gln His Pro Gly Ile Leu Lys	
10 15 20	
CTG CCS CAC GTG CGG CTG CCA CAG GCA CTG GCT AAC GGT GCC CAG TTA	243
Leu Pro His Val Arg Leu Pro Gln Ala Leu Ala Asn Gly Ala Gln Leu	
25 30 35	
TTG CTA CTT GGG AGC GGT GGG CCC ACT ATG GAG AAT CAG GTG CAA ACA	291
Leu Leu Leu Gly Ser Ala Gly Pro Thr Met Glu Asn Gln Val Gln Thr	
40 45 50	
CTG ACC AGT TAT CTC TGG AGC AGA CAT TTG CCT GTA GAG CCA GAS GAG	339
Leu Thr Ser Tyr Leu Trp Ser Arg His Leu Pro Val Glu Pro Xaa Glu	
55 60 65	

TTG CAA AGA CGG GCT ARG CAT CTT GAG AAA AAA TTC CTG GAA AAC CCA 387
Leu Gln Arg Arg Ala Xaa His Leu Glu Lys Lys Phe Leu Glu Asn Pro
70 75 80 85

GAC TTA TCT CAG ACA GAG GAG AAA CTT CGT GGA GCA GGG 426
Asp Leu Ser Gln Thr Glu Glu Lys Leu Arg Gly Ala Gly
90 95

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 160..350
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 24..107
id AAC45902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 100..149
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 13..159
id H45353
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 170..268
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 281..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 268..363
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 22..147
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..267
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 200..283
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..361
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 325..391
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 140..189
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 129..321
id N40684
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 56..173
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..118
 id N40684
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 204..336
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 267..399
 id AA005400
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 58..173
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 120..235
 id AA005400
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 31..336
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq TVMSALSVAPSKA/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGTGTCCCTT GCGCGTGGAT CCGAGCGACC ATG GTG GCC CGG GTG TGG TCG CTG	54
Met Val Ala Arg Val Trp Ser Leu	
-100 -95	
ATG AGG TTC CTC ATC AAG GGA AGT GTG GCT GGG GGC GCC GTC TAC CTG	102
Met Arg Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu	
-90 -85 -80	
GTG TAC GAC CAG GAG CTG CTG GGG CCC AGC GAC AAG AGC CAG GCA GCC	150
Val Tyr Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala	
-75 -70 -65	
CTA CAG AAG GCT GGG GAG GTG GTC CCC CCC GCC ATG NAC CAG TTC AGC	198
Leu Gln Lys Ala Gly Glu Val Val Pro Pro Ala Met Xaa Gln Phe Ser	
-60 -55 -50	
CAG TAC GTG TGT CAG CAG ACA GGC CTG CAG ATA CCC CAG CTC CCA GCC	246
Gln Tyr Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala	
-45 -40 -35	
CCT CCA AAG ATT TAC TTT CCC ATC CBT GAC TCC TGG AVT GCA GGC ATC	294
Pro Pro Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Xaa Ala Gly Ile	
-30 -25 -20 -15	

ATG	ACG	GTG	ATG	TCA	GCT	CTG	TCG	GTG	GCC	CCC	TCC	AAG	GCC	CGC	GAG	342
Met	Thr	Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro	Ser	Lys	Ala	Arg	Glu	
				-10					-5						1	

TAC	TCC	AAG	GAG	GGC	TGG	GAG	TAT	GTG	AAG	GCG	CTT	GGG				381
Tyr	Ser	Lys	Glu	Gly	Trp	Glu	Tyr	Val	Lys	Ala	Leu	Gly				
		5					10					15				

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..204
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 185..271
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 289..337
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..339
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 11..341
id T93683
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..295
id AA015679
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 398..445
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AGTTTGTAGC GGACAACATG GCGGCCTTCA TGCTGGGCTC GCTGCTGCGG ACGTTCAAGC   60
AGATGGTTCC TTCATCAGCT TCAGGCCAAG TTCGAAGTCA CTATGTAGAC TGGAGAATGT   120
GGCGCGATGT GAAGAGACGA AAAATGGCCT ATGAATACGC AGATGAGAGG CTACGTATTA   180
ATTCACTCAG GAAGAATACC ATTTTGCCAA AAATTCTTCA GGATGTGGCT GATGAAGAAA   240
TTGCTDHCCT CCCCCGGGAT AGCTGTCCTG TTAGAATCAG AAATCGGTGT GTTATGACGT   300
CCCGTCCGCG TGGTGTGAAG CGGCGCTGGA GGCTTAGTCG TATAGTCTTC CGTCACTTAG   360
CTGACCATGG GCAACTTTCT GGGATCCAGC GAGCGAC ATG GTA AAT GAG CTC CAG   415
                               Met Val Asn Glu Leu Gln
                               -15
AAC CTA TNG ASC TTG CAG GGA AGC CAA GCT TGC AGT TCC ACC AAG CAA   463
Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala Cys Ser Ser Ser Lys Gln
-10                               1                               5
AGA TTT
Arg Phe                                                                    469
```

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 102..220
id T30988
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..92
id T30988
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..225
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 110..213
id T30974
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 13..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..100
id T30974
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 84..202
id HSC0CC031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..74
id HSC0CC031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 84..202
id HSC0CD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..74
id HSC0CD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..117
id R56565
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 80..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FFFSIQPFLLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```
AACACACTCC CTCTCTCTCT CTTTTTAGCA GCAACATACA AGCCGGCCAT ATTAGAGAGA    60
TGGAATAAAA GCTTCCTTA ATG TTG TAT ATG TCT TTG AAG TAC ATC CGT GCA    112
           Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala
           -20                               -15

TTT TTT TTT AGC ATC CAA CCA TTC CTC CCT TGT AGT TCT CCG CCC CTC    160
Phe Phe Phe Ser Ile Gln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu
          -10                               -5                               1

AAA TCA CCC TCT CCC GTA GCC CAC CCG ACT AAC ATC TCA GTC TCT GAA    208
Lys Ser Pro Ser Pro Val Ala His Pro Thr Asn Ile Ser Val Ser Glu
          5                               10                               15

AAT GCA CAG AGA TGC CTN NCT ACC TCG CCC TGG    241
Asn Ala Gln Arg Cys Leu Xaa Thr Ser Pro Trp
          20                               25                               30
```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..411
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 167..398
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 38..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 202..399
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 73..137
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 213..292

id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 85..133
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..192
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 280..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 293..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..411
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 273..504
id AA032534
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 107..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 200..261
id AA032534
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 110..346
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq WVIVLTSWITIFQ/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACATAACTGA AAGTAGCTAA GGCACCCCAG CCGGAGGAAG TGAGCTCTCC TGGGTCAAGG      60
CTTGGGTCTT GCCCCGCAGA CCCTGGGAC GACCCGGCCC CAGCGCAST ATG AAC CTG      118
                                     Met Asn Leu
GAG CGA GTG TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC      166
Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr
-75                               -70                               -65
CTG GGG GGG TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC      214
Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe
-60                               -55                               -50                               -45
TGG TTC TTC CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC      262
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser
-40                               -35                               -30
CAA ATC AAA GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG      310
Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
-25                               -20                               -15
GTG ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC      358
Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
-10                               -5                               1
CGC TGG GGT GCC CTH GGG GAC TAS CTC TCC TTC ACC ATA CCC CTG GGC      406
Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile Pro Leu Gly
5                               10                               15                               20
ACC CCT GAC AAC TTC TGC ACA TAC                                     430
Thr Pro Asp Asn Phe Cys Thr Tyr
25

```

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 167..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 144..359
 id T27537
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 27..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 2..137
 id T27537
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 162..380
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 89..307
 id AA057488
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 75..172
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 1..98
 id AA057488
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 175..381
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 72..278
 id H10316
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 105..174
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 1..70
id H10316
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 162..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 60..283
id T33282
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..162
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..59
id T33282
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 174..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 65..287
id R14076
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..62
id R14076
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 122..331
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

AATTGCCTGC CTGAGTCACG TGTCAGGGGG AAGCTGGAAG GCGTCGTCTCT CCTTCCCA3 60

CTCTCCTGCC TGTCGCCCAT GTTTTCAGGC CGGGTCTGGC TTGGTCTTCC CCGTAAGRA 120

A ATG GCC GGG GAG CTC CAG GGG ACC CAG GCG CCG TCG CTT CGD GGA SCT 169
Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
-70 -65 -60 -55

GGG CTG ACC AGC CAG GAC AGC GGG GTA AAC CCG AAC AAT TGT GYG CGA 217
Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg

WO 99/06548

339

PCT/IB98/01222

-50	-45	-40	
GGT AGG GAG GCC ATG GCG TCC GGC AGT AAC TGG CTC TCC GGG GTG AAT			265
Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn			
-35	-30	-25	
GTC GTG CTG GTG ATG GCC TAC GGG AGC CTG GTG TTT GTA CTG CTA TTT			313
Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe			
-20	-15	-10	
ATT TTT GTG AAG AGG CAA ATC ATG CGC TTT GCA ATG AAA TCT CGA AGG			361
Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg			
-5	1	5	10
GGA CCT CAT GTC CCT GTR GGR NCA CAA TGC CCC CAA KGT TGC TAC AAC			409
Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn			
15	20	25	
TAT CTG TAT			418
Tyr Leu Tyr			

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 91..360
id C17648
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..104
id C17648
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 93..262

id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 261..363
id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..56
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..58
id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 59..89
id W07727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 95..252
id W00492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..60
id W00492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 255..313
id W00492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..342
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 311..345
id W00492
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..362
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 64..366
id N29017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 8..70
id N29017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..359
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 121..386
id N31560
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 116..293
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```
AAACGGAGGC AGGTTGGAGC CGCTGCCGTC GCCATGACCC GCGGTAAGCA GCGTGAGCTC   60
GCCCGCCAGA AGAATATGAA AAGCAGAGC GACTCGGTTA AGGGAAAGCG CCGAG ATG   118
                                         Met
ACG GGC TTT CTG CTG CCG CCC GCA AGC AGA GGG ACT CGG AGA TCA TGC   166
Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser Cys
-55                               -50                               -45                               -40
AGC AGA AGC AGA AAA AGG CAA ACG AGA AGA AGG AGG AAC CCA AGT AGC   214
Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser Ser
-35                               -30                               -25
TTT GTG GCT TCG TGT CCA ACC CTC TTG CCC TTC GCC TGT GTG CCT GGA   262
Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro Gly
-20                               -15                               -10
GCC AGT CCC ACC ACG CTC GCG TTT CCT CCT GTA GTG CTC ACA GGT CCC   310
Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly Pro
```

-5

1

5

AGC ACC GAT GGC ATT CCC TTT GCC CTG AGT CTG CAG MGG GTC CCT TTT 358
Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro Phe
10 15 20 25
GTG
Val 361

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..459)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 565..794
id HSZ78357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..205)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 818..1021
id HSZ78357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 310..387
id AA052404
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 52..175
id H75454
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..65
id H75454
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 230..307
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AACTTCCAAG TTGTAGTGTT GTTGTTTTCA GCCTGCTGCT GCTGCTGCTA TTGCGGCTAG   60
GGGAACCGTC GTGGGAAGG ATGGTGTGCG AAAATGTGA AAAGAACTT GGTACTGTTA   120
TCACTCCAGA TACATGGAAA GATGGTGCTA GGAATACCAC AGAAAGTGGT GGAAGAAAGC   180
TGAATGAAAA TAAAGCTTTG RCTTCAAAAA AAGCCAGAAT TGAWCCATA ATG GAA GAA   238
                                         Met Glu Glu
                                         -25

WTA AGT KCT CCA CTT GTA GAA TTT GTA AAA GTT TTG TGC ACC AAC CAG   286
Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
      -20                      -15                      -10

GTT CTC ATT ACT GCC AGG GCT GTG CCT ACA AAA AAG GCA TCT GTG CGA   334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
      -5                      1                      5

TGT GTG GMA AAA AGG TTT TGG ATA CCA AAA ACT ACA AGC AAA CAT CTG   382
Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
    10                      15                      20                      25

TCT AGA TGT ATT GAT GGA ATT TCT GGC TTT CTA AAT GAT TTT ACT TTC   430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
      30                      35                      40

TGC CTT GAA TTT TCA AGG CAT AGA TGT   457
Cys Leu Glu Phe Ser Arg His Arg Cys
      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 224:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 119..361
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..120
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 124..260
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..125
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 251..309
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 101..343
id N40141
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 24..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..102
id N40141
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 122..326
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..123
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..367)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 112..354
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(73..125)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 353..405
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq LXXVVRFPVAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATTCTTTCTT GGGCAGGCTC TCTGCTGACT CAAGTTCTTC AGTTCACGAT CTTCTAGTTC 60
CAGCGATGAG TGCACGAGTG AGATCAAGAT CCAGAGGAAG AGGAG ATG GTC AGG AGG 117
Met Val Arg Arg
-15
CTM MCG AWT GTG GTT GCA TTC GTG GCT CCC GGT GAA TCT CAG CAA GAG 165
Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu Ser Gln Gln Gln

-10

-5

1

GAA CCA CCA ACT GAC AAT CAG GAT ATT GAA CCT GGA CAA GAG AGA GAA	213
Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg Glu	
5 10 15	
GGA ACA CCT CCG ATC GAA GAA CGT AAA GTA GAA GGT GAT TGC CAG GAA	261
Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln Glu	
20 25 30 35	
ATG GAT CTG GAA AAG ACT CGG AGT GAG CGT GGA GAT GGC TCT GAT GTA	309
Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp Val	
40 45 50	
AAA GAG AAG ACT CCA CCT AAT CVT AAG CAT GCT AAG ACT AAA GAA GCA	357
Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys Thr Lys Glu Ala	
55 60 65	
GGA GAT GGG CCA TTG	372
Gly Asp Gly Pro Leu	
70	

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 299..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 278..433
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 87
region 133..236
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..159
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..136
id AA100750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..347
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 355..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 348..395
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 400..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 394..423
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 5..245
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 239..337
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 244..342
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq PIVRLLSRPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TKTTTTTTAG CA ATG GCG GTT CCC GGC GTG GGG CTC TTG ACC CGT TCG AAC 51
Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn

	-35	-30	-25	
CTG TGT GCC CGG AGA AGA ACT CGA GTC CAG CGG CCT ATC GTC AGG CTT				99
Leu Cys Ala Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu				
	-20	-15	-10	
TTG AGT TGC CCA GGA ACT GTG GCC AAA GAC CTT AGG AGA GAC GAG CAG				147
Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln				
	-5	1	5	
CCT TCA GGG AGC GTG GAG ACA GGC TTT GAA GAC AAG ATT CCC AAA AGG				195
Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg				
	10	15	20	
AGA TTC TCG GAG ATG CAA AAT GAA AGA CGA GAA CAG GCA CAG CGG ACT				243
Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr				
	25	30	35	40
GTT TTA ATA CAT TGC CCA GAG AAA ATC AGT GAA AAC AAG TTT CKK AAA				291
Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys				
	45	50	55	
TAT TTA TCC CAA TTT GGA CCT ATT AAT AAT CAT TTC TTC TAT GAA AGC				339
Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser				
	60	65	70	
TTT GGT CTC TAT GCT GTC GTA GAA TTT TGC CAA AAG GAA AGC ATA GGT				387
Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly				
	75	80	85	
TCA CTG CAG AAT GGG ACT CAT ACT CCA AGC ACG GCC ATG GAG ACT GCA				435
Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala				
	90	95	100	
ATT CCA TTC AGA TCA CGT TCT TCA				459
Ile Pro Phe Arg Ser Arg Ser Ser				
	105	110		

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 43..253
id AA017309

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 93..124
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 28..59
 id AA017309
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(126..250)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..125
 id T52392
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 21..200
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.8
 seq LVILSLKSQTLDA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AGTAAGTCCC CCCGCCTCGC ATG ATG GCT GCG GTG CCG CCG GGC CTG GAG CCG      53
      Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
      -60              -55              -50

TGG AAC CGT GTG AGA ATC CCT AAG GCG GGG AAC CCG ACC GCA GTG ACA      101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
      -45              -40              -35

GTG CAG AAC CCC GGC GCG GCC CTT GAC CTT TGC ATT GCA GGT GTA ATT      149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
      -30              -25              -20

AAA GAA TGC CAT CTC GTC ATA CTG TCG CTG AAG AGC CAA ACC TTA GAT      197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
      -15              -10              -5

GCA GAA ACA GAT GTG TTA TGT GCA GTC CTT TAC AGC AAT CAC AAC AGA      245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
      1              5              10              15

ATG GGC CGC CAC AAA CCC CAT TTG GCC CTC AAA CAG GTT GAG CAA TGT      293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
      20              25              30

TTA AAG CGT TTG ARA AAC ATG AAT TTG GAG GGC GGC      329
Leu Lys Arg Leu Xaa Asn Met Asn Leu Glu Gly Gly
      35              40

```

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..347
id AA023764
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 145..384
id C03036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..80
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 2..71
id C03036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..193
id R08519
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 193..263
id R08519
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..109

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8
seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

AAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA      49
Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly
          -30                      -25

GAC TCA GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT      97
Asp Ser Gly Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn
-20          -15                      -10                      -5

CAA GTG CTG GGA AAT CCA TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC      145
Gln Val Leu Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val
          1                      5                      10

AGA GTK CAT GAT TAC AAA GAA GGA ACC CCA GAA GAG AAG ACC TAC TAC      193
Arg Val His Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr
          15                      20                      25

ATA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC AGC GTG      241
Ile Glu Leu Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val
          30                      35                      40

AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATW NYC      289
Lys Ser Thr Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa
          45                      50                      55                      60

GTA CAC GAC TTA ACV SAT GGG AAG TCC TCC CAA AAM TTG CGN CGT TGG      337
Val His Asp Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp
          65                      70                      75

TCA TTG GAA GCT CTC AAC AGG GAT TTG GTG CCA ACT GGA GTC TTG GTG      385
Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val
          80                      85                      90

```

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 12..219

id R19497
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 236..270
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 219..253
id R19497
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..185
id H75597
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 236..270
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 184..218
id H75597
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..179
id H93398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 236..270
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 178..212
id H93398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 98..270
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..173
id HUM030E11B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..127
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 118..244
id AA280273
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
CGGTCCGCGC CATCAGGCCG GAGATAGCGG CGAGGTCCGC TTTCAGTGT ATG GTT TTC    58
                                   Met Val Phe
                                   -30

CCT GCC AAA CGG TTC TGC TTG GTG CCA TCC ATG GAG GGC GTG CGC TGG    106
Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly Val Arg Trp
   -25                      -20                      -15

GCC TTT TCC TGC GGC ACT TGG CTG CCG AGC CGA GCC GAA TGG CTG CTK    154
Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu Trp Leu Leu
   -10                      -5                      1

RCA GTG CGA TCG ATT CAG CCC GAG GAG AAG GAG CGC ATT GGC CAG TTC    202
Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile Gly Gln Phe
   5                      10                      15                      20

GTC TTT GCC CGG GAC GCT AAG GCA GCC ATG GCT GGT CGT CTG ATG ATA    250
Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg Leu Met Ile
           25                      30                      35

AGG AAA TTA GTT GCA GAG AAT CGA                                274
Arg Lys Leu Val Ala Glu Asn Arg
           40
```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrenals

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 90..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 105..223

id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 18..115
id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 71..189
id T08849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..81
id T08849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..83
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 71..139
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..206
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 140..139
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..203
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 92..189
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..110
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..92
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 141..179
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSLVLTTC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ACTTTCCCAA G ATG GCG TCG AAG ATA GGT TCG AGA CGG TGG ATG TTG CAG	50
Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln	
-25 -20 -15	
CTG ATC ATG CAG TTG GGT TCG GTG CTG CTC ACA CGC TGC CCC TTT TGG	98
Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp	
-10 -5 1	
GGC TGC TTC AGC CAG CTC ATG CTG TAC GGT GAG AGG GGT GAG GCA CGC	146
Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg	
5 10 15	
CGG AAG CCC GAC ATC CCA GTG CCT TAC CTG TAT TTC GAG ATG CGG GCA	194
Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala	
20 25 30 35	
GCC GTG CTG TGC GCG CGG	212
Ala Val Leu Cys Ala Arg	
40	

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..272
id W52056
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAGAACTGCG TCTGCGGACC CAGGCGCGGG TTCCCGGAGG ACAGCCACCA AGCGATGCTG    60
CCGCCGCCGT TTCTGATTG GTTGTGGGTG GCTACCTCTT CGTTCTGATT GSCCGCTAGT    120
GAGCAAG ATG CTG AGC AAG GGT CTG AAG CGG AAA CGG GAG GAG GAG GAG    169
Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Gln Gln Glu Glu
      -30                -25                -20

GAG AAG GAA CCT CTG GCA GTC GAC TCC TGG TGG CTA GAT CCT GGC CAC    217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
      -15                -10                -5

GCA GCG GTG GCA CAG GCA CCC CGG GGC GTG GCC TCT AGC TCC CTC TTT    265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
      1                5                10                15

GAC CTC TCA GTG CTC AAG CTC CAC CAC AGC CGC GGG    301
Asp Leu Ser Val Leu Lys Leu His His Ser Arg Gly
      20                25

```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 88..277
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 36..89
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 345..379
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..31
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 313..344
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..316
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 279..312
id W02951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 81..293
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 292..363
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 291..367
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 24..31
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 93..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 79..367
id R91018
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 14..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..80
id R91018
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id W19557
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 13..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..81
id W19557
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 305..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 221..366
id W19557
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 282..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq SLAAPALTLLGHWG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

AAGGAACGAG ATGSCGGTTC TCTGGAGGCT GAGTGCCGTT TCGGSGGCC TAGGAGGCCG 60
AGCTCTGTTG CTCGAACTC CAGTGGTCAG AMCCTGCTCA TATCTCAGCA TTTCTTCAGG 120
ACCGACCTAT CCGAGAATGG TGTGGAGTGC AGCACATACA TTGTCAACCG AGCCACCATT 180
CTGGCTCCAA GGSTGCATCT CTCCACTGGA CTAGCGAGAG TTTTTCAGT GTTTTGCTCC 240

TGGGTCGTGCT TCCGGCTGCT TATTTGAATC CTTGCTCTGC G ATG GAC TAT TCC CTG 296
 Met Asp Tyr Ser Leu
 -15

GCT GCA GCC CTC ACT CTT CAT GGT CAC TGG GGC CTT GGA CAA GTT GTT 344
 Ala Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val
 -10 -5 1 5

ACT GAC TAT GTT CAT GGG GAT GCC TTG CAG AAA GCT 380
 Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala
 10 15

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
 region 128..338
 id HUM090D04B
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
 region 1..134
 id HUM080D04B
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
 region 339..399
 id HUM080D04B
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 407..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 397..435
id HUM080D048
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 127..263
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..133
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 263..338
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 339..378
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 374..403
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 127..339
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..143

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..134
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..397
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 339..388
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 407..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 396..426
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..299
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 135..296
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..141
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 292..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 290..346
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 402..441
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 400..446
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 138..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 94..282
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 44..143
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..100
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 348..408
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 306..366
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 181..396
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq LSLXASYIFGISG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```

AGTTTTCAGG ARATTGGAA GGTGCCGCAG TAGTTGGAGT CTAAGGACTC GTGACAATCT   60
TCGGGTGCCC TTCGAGAGAA AAGGGGAGGA TGCCACTGGA GTCATCCTCT TCAATGCCAC   120
TATCCTTCCC ATCTBYBYTD RCCCTCRGTA CCACACAATA CTAACCCTTC CCCTNCTCTG   180
ATG TCT TAC ATC ACC TCC CAG GAG ATG AAG TGT ATT CTT CAC TGG TTT   228
Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
   -70                               -65                               -60
GCC AAT TGG TCA GGT CCC CAG CGT GAA CGT TTC CTA GAG GAC CTG GTA   276
Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
   -55                               -50                               -45
GCT AAG GCA GTG CCA GAA AAA TTA CAA CCA ATG CTG GAT AGT CTG GAG   324
Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
   -40                               -35                               -30                               -25
CAG CTT AGT GTG TCT GGG GCA GAC GAC CAC CTT CTA TCT TTG WGT GCC   372
Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
   -20                               -15                               -10
AGC TAC ATC TTT GGG ATC AGT GGT TTC GAG GCT GGG GCT GAG CAG GAG   420
Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
   -5                               1                               5

```

CGC AAT GAA TTT GTC AGA CAG TCG
Arg Asn Glu Phe Val Arg Gln Ser
10 15

444

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 6..366
id W31793
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..353
id AA056667
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 4..342
id AA131953
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..334
id H10262
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..406
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..330
id W95790
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 200..427
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
AAGACGAGGT CATGAATCAT GTGACGGTGG CTTGAGGAGG AACCTGTCTT TAAAGCTGTC    60
CCTGAAGTGA CAGCGGAGAG AACCAGGCAG CCCAGAAACC CCAGGCGTGG AGATTGATCC    120
TGCGAGAGAA GGGGGTTCAT CATGGCGGAT GACCTAAAGC GATTCTTGTA TAAAAAGTTA    180
CCAAGTGTG AAGGGCTCC ATG CCA TTG TTG TGT CAG ATA GAG ATG GAG TAC    232
      Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
      -75                      -70

CTG TTA TTA AAG TGG CAA ATG ACA ATG CTC CAG AGC ATG CTT TGC GAC    280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65                      -60                      -55                      -50

CTG GTT TCT TAT CCA CTT TTG CCC TTG CAA CAG ACC AAG GAA GCA AAC    328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
      -45                      -40                      -35

TTG GAC TTT CCA AAA ATA AAA GTA TCA TCT GTT ACT ATA ACA CCT ACC    376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
      -30                      -25                      -20

AGG TGG TTC MAT TTA ATC GTT TAC CTT TGG GTG GTG AGT TTC ATA GCC    424
Arg Trp Phe Met Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
      -15                      -10                      -5

AGC AGC AGT    433
Ser Ser Ser
1
```

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 39..179
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 161..261
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..219
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 22..224
id W07092
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 140..377
id W72958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 16..255
id W24219
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 16..253
id AA040714
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..110
- (C) IDENTIFICATION METHOD: Von Heljne matrix
- (D) OTHER INFORMATION: score 4.7
seq SVMGVOLLIPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAGGACCCA GAAGTAGGGT TTTGGCCTAG GTAACGGGGC AGAG ATG TGG TTC GAG      56
                                     Met Trp Phe Glu
                                     -20

ATT CTC CCC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT CCA GGA      104
Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile Pro Gly
      -15                      -10                      -5

CTG GCT ACT GCG TAC ATC CAC ARG TTC ACT AAC CGG GGC AAG GAA AAA      152
Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg Gly Lys Glu Lys
      1                      5                      10

AGG GTT GCT CAT TTT GGG TAT CAC TGG AGT CTG ATG GAA AGA GAT AGG      200
Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met Glu Arg Asp Arg
      15                      20                      25                      30

CGC ATC TCT GGA GTT GAT CGT TAC TAT GTG TCA AAG GGT CCA GGG      245
Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys Gly Pro Gly
      35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Prostate

- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 204..351
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 93
region 162..309
id AA017973
est

- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 204..351
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 93
region 181..323
id AA021972
est

- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 204..351
 - (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 181..328
id AA013987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 168..315
id AA014054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 184..331
id W80073
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 205..342
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```
AGTTTAGCGA CCGGACCCGA AACGGGAAG TTGTCTTGTG TGGAGAGGTT AGTAAAGCAG      60
CGCGCGCGTC ACCAGAGTCG TTTCTCTTCG GAGTCTTAGG TGATCGAGGG TGTGCCCAGG     120
GGSCGGACTT GTTTGCGCCT CCCGTTCCCT CCCAATTTC AAACGTGTCA CCCC GGCGCC      180
GACGGCCCTG TGCAGGGGAA GCAG ATG GAG TTC AAG CTG GAG GCT CAT CGC          231
              Met Glu Phe Lys Leu Glu Ala His Arg
              -45                               -40
ATC GTC AGC ATC TCT CTG GGC AAG ATC TAC AAC TCG CGG GTC CAG CGC          279
Ile Val Ser Ile Ser Leu Gly Lys Ile Tyr Asn Ser Arg Val Gln Arg
              -35                               -30                               -25
GGC GGC ATC AAG CTG CAT AAG AAC CTC CTG GTC TCG CTG GTG CTG CGC          327
Gly Gly Ile Lys Leu His Lys Asn Leu Leu Val Ser Leu Val Leu Arg
              -20                               -15                               -10
ASG CCC GCC AAG TCT ACC CGA GCG GGG                                      354
Xaa Pro Ala Lys Ser Thr Arg Ala Gly
              -5                               1
```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..179
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 179..333
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..363
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..285
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 338..381
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 307..336

id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 27..337
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 347..382
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..216
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 271..332
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 216..278
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 332..376
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..368
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..310
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 370..414
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 311..355
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IASGLGLXLDCT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCTAGCCC CGCCCCAGGC GAGGGCGCCG CACCCACACC GCGCTGCGCA GTTTTGTTC 60
GCTCCAGCTG TTCGAAGGTG ATCCAGACGC AAG ATG GCT GTC CTC TCT AAG GAA 114
Met Ala Val Leu Ser Lys Glu
-95

TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC 162
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
-90 -85 -80 -75

CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG 210
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
-70 -65 -60

TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC 258
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
-55 -50 -45

TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CSC TTC 306
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Xaa Phe
-40 -35 -30

TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT 354
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
-25 -20 -15

GGC CTG GGC TTG DCN CTG GAT TGT TGG ACG AGT TCT TTA TGC TTA TGG 402
Gly Leu Gly Leu Xaa Leu Asp Cys Trp Thr Ser Ser Leu Cys Leu Trp
-10 -5 1 5

CTA TTA CAC GGG CCG GGG 420
Leu Leu His Gly Pro Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 28..227
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..200
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 265..310
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 233..283
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 227..263
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 201..237
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 352..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 328..361
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(259..406)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 123..272
 id N93600
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(85..207)

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 325..447
id N93600
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(202..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 117..323
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(116..153)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 375..412
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(167..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 324..359
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(253..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 123..273
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(208..251)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 280..323
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(163..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 329..368
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(90..125)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 411..446
 id N93603
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 272..397
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq RIPS LPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

AAAAGGAAAG AGGTYSGGAG CGCTCGCGAG ATCTCGGACC ACCCAACCTG AAAGGTGCTT   60
AGGAAGTTGA AAGGCCCAGA GGAGGCCTCC GGGCAAATGG CCGGAGCTGG ACCGACCATG  120
CTGCTACGAG AAGAGAATGG CTGTTGCAST CGGCGTCAGA GCAGCTCCAG TGCCGGGGAT  180
TCGGACGGAG AAGCGGAGGA CTCGGCGGCT GAGCGCGCCC GACAGCAGCT AGAGGCGCTG  240
CTCAACAAGA CTATGCGCAT TCGCATGACA G ATG GAC GGA CAC TGG TCG GCT      292
                               Met Asp Gly His Trp Ser Ala
                               -40

GCT TTC TCT GCA CTG ACC GTG ACT GCA ATG TCA TCC TGG GCT CGG CGC      340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                               -30                               -25                               -20

AGG AGT TCC TCA AGC CGT CGG ATT CCT TCT CTG CCG GGG AGC CCC GTG      388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
-15                               -10                               -5

TGC TGG GGC TGG CCA TGG
Cys Trp Ala Trp Pro Trp
1

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Liver

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 56..207

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 20..171
id N41898
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 38..176
id H69272
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLLLRFLASVIS/RK

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ACTTGACAGG CAGGGAGGGC TAGGCTGTGC ATCCCTCCGC TCGCATTGCA GGGAG ATG	58
Met	
GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT GTC ATC TCC AGG	106
Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser Arg	
-15 -10 -5 1	
AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC AGA GCC CTG CAG	154
Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu Gln	
5 10 15	
ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA CCC AAC CCA GCC	202
Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro Ala	
20 25 30	
CGG ACG	208
Arg Thr	
35	

(2) INFORMATION FOR SEQ ID NO: 239:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: cDNA

(12) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(13) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 103..322
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 4..115
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..398
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 336..377
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..337
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..391
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..335
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..134
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..123
id AA054941
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 191..283
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..277
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 117..184
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 361..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 360..397
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 97..316
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..108
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 330..371
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(153..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 108..255
id H72704
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(291..343)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 64..116

id H72704
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(101..151)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 259..309
id H72704
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(357..398)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 9..50
id H72704
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 311..385
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq FLLLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
AGACGTGTTTCCCGGTGGC GGASGGCGGA TTAGCCTTCG CGGGGCATAA TGGAGCTCGA 60
GGCCATGAGC AGATATACCA GCCAGTGAA CCCAGCTGTC TTCCCCCATC TGACCGTGGT 120
GCTTTTGGCC ATTGGCATGT TCTTACCGC CTGGTTCTTC GTTTACGAGG TCACCTCTAC 180
CAAGTACACT CGTGATATCT ATAAAGAGCT CCTCATCTCC TTAGTGGCCT CACTCTTCAT 240
GGGCTTTGGA GTCTCTTCC TGCTGCTCTG GGTGGGCATC TACGTGTGAG CACCCAAGGG 300
TAACAACCAG ATG GCT TCA CTS AAA CCT GCT TTT GTA AAT TAC TTT TTT 349
Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe
-25 -20 -15
TTA CTG TTG CTG GAA GTG TCC CAC CTG CTG CTC ATA ATA AAT GCA GAA 397
Leu Leu Leu Leu Glu Val Ser His Leu Leu Ile Ile Asn Ala Glu
-10 -5 1
GGG
Gly
5 400
```

(2) INFORMATION FOR SEQ ID NO: 240:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..396

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 202..372
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 27..162

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 158..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 213..292
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 157..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..192
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 293..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 167..337
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155

id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 226..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 177..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 156..386
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
AAAAACGTCC ATAACTGAAA GTAGCTAAGG CACCCCAGCC GGAGGAAGTG AGCTCTCCTG   60
GGGCGTGGTT GTTCGTGATC CTTGCATCTG TTAAGTAGGG TCAAGGCTTS GGTCTTGCCC   120
CGCAGACCCT TGGGACGACC CGGCCCCAGC GCAST ATG AAC CTG GAG CGA GTG   173
                               Met Asn Leu Glu Arg Val
                               -75
TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC CTG GGG GGG   221
Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr Leu Gly Gly
-70                               -65                               -60
TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC TGG TTC TTC   269
Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe Trp Phe Phe
-55                               -50                               -45                               -40
CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC CAA ATC AAA   317
Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser Gln Ile Lys
-35                               -30                               -25
GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG GTG ATA GTG   365
Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp Val Ile Val
-20                               -15                               -10
CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC   395
Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
-5                               1
```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 170..205
id AA090974
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq AVASSFFCASLES/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```

ATTTTTTCT TGCTCGTGGG CTCGGACGAG TACGGAGCGC CTGCAGGGAC AGCCTGGATA   60
AAGGCTCACT TG ATG GCT CAG TTG GGA GCA GTT GTG GCT GTG GCT TCC AGT   111
      Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser
      -20                      -15                      -10

TTC TTT TGT GCA TCT CTC TTC TCA GCT GTG CAC AAG ATA GAA GAG GGA   159
Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly
      -5                      1                      5

CAT ATT GGG GTA TAT TAC AGA GGC GGT GTG
His Ile Gly Val Tyr Tyr Arg Gly Gly Val   189
      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 16..262
id AA044042
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 46..78
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..33
id AA044042
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 75..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 6..239
id AA127902
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..216
id AA056679
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(104..308)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 246..450
id W93399
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 126..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 2..184
id H39528
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 122..196
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```
GCGAAGGTTG TCGGGATCCG CGGCAGCAGC GGCTGCTTGA GATCTGTTTC TGGGGCCTCT   60
GGCGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG GTACACTGAT GCTGAAGTAC   120
T ATG AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT TTT ATG   169
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25                -20                -15                -10

GTC CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC   217
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
-5                1                5

AGC CCT GTT TTC CAA ATA CCT AAA AAC GAC GAC ATT COT GAG CAA GAT   265
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
10                15                20

AGT CTG GGA CTT TCA AAT CTT CAG AAG AGC CAA ATC CAG GGG ATA CTG   313
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
25                30                35
```

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 33..232
id AA088497
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 341..409
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VFCLLSIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AGTCGTTGCC ATSGATCCTG GGGACGACTG GCTGGTGGAA TCCTTGCGCT TGTAATCGT 60
ACCAGGATTT CTATGCATTC GACCTGTCAG GAGCCACTCG AGTCCTTGAA TGGATTGATG 120
ACAAAGGAGT CTTTGTGCT GGCTATGAAA GCCTGAAAAA GAATGAAATT CTCATCTGA 180
AATTACCTCT CAGACTTTCT GTAAAGGAAA ACAAGGGCTT ATTCCCAGAA AGAGATTTC 240
AAGTGCGCCA TGGAGGATTT TCAGACAGGT CTATCTTTGA TCTAAAGCAT GTGCCACATA 300
CCAGGTATGG TCAATTTTGT GATCCAGCCA TCCACACAGG ATG GGA TGG GAT GGC 355
Met Gly Trp Asp Gly
-20
TGC AAA TGC CTG GGG GTA TTC TGC CTC CTC ATC TCC ATT CCC ACC CCC 403
Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile Ser Ile Pro Thr Pro
-15 -10 -5
TCA GCA CAC CTG 415
Ser Ala His Leu
1

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..451
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 122..417
id AA085629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 14..114
id AA085629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..259
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 134..237
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 29..126
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 254..294
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 15..112
id H35088
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 156..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 63..252
id HUM111153
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..365
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq ILAHLRLGLPIHA/DP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

AGAGATTGAA G ATG GCG GCT TCT CAG GCG GTG GAG GAA ATG CGG ACC GCG	50
Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala	
-115 -110	
TGG TTC TGG GGG AGT TTG GGG TTC GCA ATG TCC ATA CTA CTG ACT TTC	98
Trp Phe Trp Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe	
-105 -100 -95 -90	
CCG GTA ATT ATT CCG GTT ATG ATG ATG CCT GGG ACC AGG RMC GGY TTC	146
Pro Val Thr Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe	

-85	-80	-75	
GAA GRA AGA AWT TTC CGT GTG GAT GTA GTA CAC ATG GAT GAA AAC TCA Glu Xaa Arg Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser	-70	-65	-60
CTG GAG TTT GAC ATG GTG GGA ATT GAC GCA GCC ATT GCC AAT GCT TTT Leu Glu Phe Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe	-55	-50	-45
CGA CGA ATT CTG CTA GCT GAG GTG CCA ACT ATG GCT GTG GAG AAG GTC Arg Arg Ile Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val	-40	-35	-30
CTG GTG TAC AAT AAT ACA TCC ATT GTT CAG GAT GAG ATT CTT GCT CAC Leu Val Tyr Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His	-25	-20	-15
CGT CTG GGG CTC ATT CCC ATT CAT GCT GAT CCC CGT CTT TTT GAG TAT Arg Leu Gly Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr	-5	1	5
CGG AAC CAA GGA GAT GAA GAA GGC ACA GAG ATA GAT ACT CTA CAG TTT Arg Asn Gln Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe	10	15	20
CGT CTC CAG GTC AGA TGC ACT CGG Arg Leu Gln Val Arg Cys Thr Arg	25	30	
			194 242 290 338 386 434 458

(2) INFORMATION FOR SEQ ID NO: 245:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(VI) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(18) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..172
id AA156837
est

(19) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 234..316

id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 189..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 172..239
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..49
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..206
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 236..318
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 207..241
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 44..209
id AA181144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 235..317
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..48
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 225..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 209..240
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 185..334
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 169..318
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 46..169
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..50
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..219
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..205
id W04828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 252..334
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 236..318
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 341..380
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 323..362
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 221..256
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 206..241
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 12..242
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq FEARIALLPLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATACTGCGAG T ATG GCG GCG TCA AAG GTG AAA CAG GAC ATG CCT CCG CCG	50
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro	
-75 -70 -65	
GGG GGC TAT GGG CCG ATC GAC TAC AAA CGG AAC TTR CCG CGT CGA GGA	98
Gly Gly Tyr Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly	
-60 -55 -50	
CTG TCG GCG TAC ACC ATG CTG GCC ATA GGG ATT GGA ACC CTG ATC TAC	146
Leu Ser Gly Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr	
-45 -40 -35	
GGG CAC TGG AGC ATA ATG AAG TGG AAC CGT GAG CGC AGG CGC CTA CAA	194
Gly His Trp Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln	
-30 -25 -20	
ATC GAG GAC TTC GAG GCT CGC ATC GCG CTG TTG CCA CTG TTA CAG GCA	242
Ile Glu Asp Phe Gly Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala	
-15 -10 -5	
GAA ACC GAG CCG AAG ACC TTG CAG ATG CTT CCG GAG AAC CTG GAG GAG	290
Gln Thr Asp Arg Lys Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu	
1 5 10 15	
GGG GCG ATC ATC ATG MAG GAC GTS CYC GAC TGG AAG GTG GGG RAA KVV	338
Gln Ala Ile Ile Met Lys Asp Val Lys Asp Trp Lys Val Gly Lys Lys	

20

25

30

GHT GTT CCA CAC AAC CCG CTG GGT GCC CCC CTT GAT CGG GGA GCT
Xaa Val Pro His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
35 40 45

383

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 54..267
id AA027968
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 94..278
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..99
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 21..265
id HSC0SD021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..299

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..259
 id T31694
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 116..274
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 61..219
 id R38457
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 55..107
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..53
 id R38457
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 273..307
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 219..253
 id R38457
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 164..289
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq VLFFTGWWIIIDA/AV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AATCCGCGAC TGAGCCGGGT GGATGGTACT GCTGCATCCG GGTGTCTGGA GGCTGTGGCC   60
GTTTTGTTTT CTTGGCTAAA ATCGGGGGAG TGAGGCGGGC CGGCGCGGCG CGACACCGGG   120
CTCCGGAACC ACTGCACGAC GGGGCTGGAC TGACCTGAAA AAA ATG TCT GGA TTT   175
                               Met Ser Gly Phe
                               -40
GTA GAG GGC TTG AGA TGC TCA GAA TGC ATT GAC TGG GGG GAA AAG CGC   223
Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp Gly Glu Lys Arg
-35 -30 -25
AAT AAT ATT GCT TCC ATT GCT GCT GGT GTA CTA TTT TTT ACA GGC TGG   271
Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe Phe Thr Gly Trp
-20 -15 -10
TGG ATT ATC ATA GAT GCA GCT GTT ATT TAT CCC ACC CGG   310
Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr Arg

```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 73..353
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 42..71
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 145..290
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 47..143
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 319..374
id AA159550

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 33..68
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 10..45
 id AA159550
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 225..356
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LVFLTFLSIPSEV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```

AAGGTGCTCG TCATGCGCAA TGTGGCGCTG CGGCGGGCGG CAGGGCCTGT GTGTGCTGAG   60
GCGGCTGAGC GGCGGACATG CACACCACAG AGCGTGGCGA TGGACAGTA ACCGGGCTTG   120
TGAGAGGGCT CTGCAGTATA AACTAGGAGA CAAGATCCAT GGATTCACCG TAAACCAGST   180
GACATCTGTT CCGGAGCTGT TCCTGACTGC AGTGAAGCTC ACCC ATG ATG ACA CAG   236
                               Met Met Thr Gln
GAG CCA GGT ATT TAC ACC TGG CCA GAG AAA ACA CGA ATA ATC TGT TCA   284
Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg Ile Ile Cys Ser
-40                               -35                               -30                               -25
GCG TGC AST TCC GTA CCA CTC CCA TGG ACA GTA CTG GTG TTC CTC ACA   332
Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu Val Phe Leu Thr
                               -20                               -15                               -10
TTC TTG AGC ATA CCG TCC TTT GTG GGT CTC AGA AAT ATC CCG GCA GAG   380
Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn Ile Arg Ala Glu
                               -5                               1                               5
ACC TTT CTT CAA AAT GTT
Thr Phe Leu Gln Asn Val   396
10

```

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (E) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(53..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 444..585
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(227..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 311..408
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 230..309
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 183..226
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 75..153
id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(275..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 156..205
id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 32..71

id R06263
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 286..342
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 89..141
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 242..233
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..44
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 351..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 312..367
id AA159107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 406..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 371..403
id AA159107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..225
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 166..193
id AA159107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(171..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 313..466
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(328..406)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 232..310
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(408..446)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 190..228
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 39..80
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq FLTALLWRCRIPG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AGCGGAGACG CAGAGTCTTG AGCAGCGCGN CAGGCACC ATG TTC CTG ACT GCG CTC    56
                               Met Phe Leu Thr Ala Leu
                               -10

CTC TGG CGC GGC CGC ATT CCC GGC CGT CAG TGG ATC GGG AAG CAC CGG    104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
      -5                      1                      5

CGG CCG CGG TTC GTG TCG TTG CGC GCC AAG CAG AAC ATG ATC CGC CGC    152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
      10                      15                      20

CTG GAG ATC GAG GCG GAG AAC CAT TAC TGG CTG AGC ATG CCC TAC ATG    200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
      25                      30                      35                      40

ACC CGG GAG CAG GAG CGC GGC CAC GCC SGG TTG CGC AGG AGG GAG GCC    248
Thr Arg Glu Glu Glu Arg Gly His Ala Xaa Leu Arg Arg Arg Glu Ala
      45                      50                      55

```

TTC GAG GCS ATA AAG GCG GCC GCC ACT TCC AAG TTC CCC CCG CAT AGA	296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg	
60 65 70	
TTC ATT GCG GAC CAG CTC GAC CAT CTC AVK VGT CAC CAA GAA ATG GTC	344
Phe Ile Ala Asp Gln Leu Asp His Leu Xaa Xaa His Gln Glu Met Val	
75 80 85	
CTA ATC CTG AGT CGT CAC CCT TGG ATT TTA TGG ATC ACG GAG CTG ACC	392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr	
90 95 100	
ATC TTT ACC TGG TCT GGA CTG AAA AAC TGT AGC TTG TGT GAA AAT GAG	440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu	
105 110 115 120	
CTT TGG ACC AGT CTT TAT	458
Leu Trp Thr Ser Leu Tyr	
125	

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..331
id W56872
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..291
id W31727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..354
id W16469
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..400
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..356
id N31028
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..354
id W16470
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..389
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```

AACTTGCTCT GAGACAGGTG CGGCAAGTCT ACTGCGGGCT GGTCCGGGCT CCTCAGGTTT 60
AGACCCGACC GTTATCCAGT CGGTTCTGTTG AGAGGAGAGG TGSACTTTAC AGGTCCCCG 119
ATG AAC CAA GAG AAC CCT CCA CCA TAT CCA GGC CCT GGT CCA ACG GCC 167
Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
-90 -85 -80 -75
CCA TAC CCA CCT TAT CCA CCA CAA CCA ATG GGT CCA GGA CHT ATG GGG 215
Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly
-70 -65 -60
GGA CCC TAC CCA CCT CCT CAA GGG TAC CCC TAC CAA GGA TAC CCA CAG 263
Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln
-55 -50 -45
TAC GGC TGG CAG GGT GGA CCT CAG GAG CCT CCT AAA ACC ACA GTG TAT 311
Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
-40 -35 -30
GTG GTA GAA GAC CAA AGA AGA GAT GAG CTA GGA CCA TCC ACC TGC CTC 359
Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
-25 -20 -15
ACA GCC TGC TGG ACG GCT CTC TGT TGC TGC TGT CTC TGG 398
Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp
-10 -5 1

```

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..332
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..59
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 329..368
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..273
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 234..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 274..321
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..47
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 319..357
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..264
id W01758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 261..300
id W01759
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 53..249
id W57829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..49
id W57829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..214
id HUM417E03B

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

AAGTTCGGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC AGG TCT      49
Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser
               -50                      -45

CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA CAT TCG GTG      97
Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val
-40               -35                      -30

CTT TTA CCT ACC TAC AAC GAG CGC GAR GAA CTG CCG CTC ATC GTG TGG     145
Leu Leu Pro Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp
-25               -20                      -15                      -10

CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA ATT ATA     193
Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile
               -5                      1                      5

ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT GAA CAG     241
Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln
               10                      15                      20

TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA CGA GAG     289
Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu
               25                      30                      35

AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CAT GGA ATG RAA ACA TGC     337
Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys
               40                      45                      50                      55

CAC AGG RAA CTA CAT CAT TAT TAT GGA TGC                             367
His Arg Xaa Leu His His Tyr Tyr Gly Cys
               60                      65

```

(2) INFORMATION FOR SEQ ID NO: 251:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(VI) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..408
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 61..399
id AA114853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..68
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..60
id AA114853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..391
id W23545
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 42..381
id AA069652
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..68
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..41
id AA069652
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 8..333
id AA084987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..347
id AA101916
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 303..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CPTCLCAPSXXWG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```

ATCCGGTGCA CGCGAGTSTT CTGAAACGTC AGCTGCGCTC CCCTAGGAGT GCTGAGCCCG   60
CGGAACCGCA GCCATGACTG AGGCTGATGT GAATCCAAAG GYCTATCCCC TTGCCGATGC   120
CCACCTCACC AAGAAGCTAC TGGACCTCGT TCAGCAGTCA TGTAATAATA AGCAGCTTCG   180
GAAAGGWGCC AATGAGGCCA CCAAAACCCT CAACAGGGGC ATCTCTGAGT TCATCGTGAT   240
GGCTGCAGAC GCCGAGCCAC TGGAGATCAT TCTGCACCTG CCGCTGCTGT GTGAAGACAA   300
GA ATG TGC CCT ACG TGT TTG TGC GCT CCA AGC AVN SCC TGG GGA GAG   347
  Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu
      -10                -5                1
CCT GTG GGG TCT CCA GGC CTG TCA TCG CCT GTT CTG TCA CCA TCA AAG   395
  Pro Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys
      5                10                15
AAG GCT CGC AGC
  Lys Ala Arg Ser   407
      20

```

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 34..153
id N52621
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..38

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..31
id N52621
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 5..152
id AA157163
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 10..66
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq AVAASAASGQAEQ/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
ACTTCTAAG ATG GCT GCC GCT ACC GGT GCG GTG GCA GCC TCG GCC GCC TCG    51
Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser
           -15                      -10

GGT CAG GCG GAA GST AAA AAG ATC ACC GAT CTG CGG GTC ATC GAT CTG    99
Gly Gln Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu
-5                      1                      5                      10

AAG TCC GAG CTG AAG CGG CGG AAC TTA GAC ATC ACC GGA GTC AAG ACC    147
Lys Ser Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr
           15                      20                      25

GTG CTC ATC TCC CGA CTA AGG    168
Val Leu Ile Ser Arg Leu Arg
           30
```

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..343

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..306
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..103
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 340..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 304..397
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..388
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..401
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..356
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..389
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 82..339
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 50..139
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..90
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 387..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 338..384
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 126..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 75..382
 id H29689
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 23..73
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq SLLXRVSVTAVAA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

ATTCCTCCTG CCCGTAGTAG CC ATG GCG GCC ATG AGT TCG TTG CAG CGG GTT	52
Met Ala Ala Met Ser Leu Leu Xaa Arg Val	
-15 -10	
TCG GTT ACT GCG GTG GCA GCT CTG TCT GGC CGG CCC CTT GCC ACY NGC	100
Ser Val Thr Ala Val Ala Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa	
-5 1 5	
CTC GGA TTT GGG GGC TTC CTC ACT CGT GGC TTT CCG AAG GCT GCT GCT	148
Leu Gly Phe Gly Gly Phe Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala	
10 15 20 25	
CCT GTT CGA CAG AGT GGA GAC CAT GGG AAA AGA CTA TTT CTC ATC AGA	196
Pro Val Arg His Ser Gly Asp His Gly Lys Arg Leu Phe Val Ile Arg	
30 35 40	

WO 99/06548

408

PCT/IB98/01222

CCT TCT AGA TTC TAT GAC AGG CGT TTT TTG AAG TTA TTG AGA TTC TAC	244
Pro Ser Arg Phe Tyr Asp Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr	
45 50 55	
ATT GCA TTG ACT GGG ATT CCA GTA GCA WTT TTC ATA ACT CTG GTG AAT	292
Ile Ala Leu Thr Gly Ile Pro Val Ala Xaa Phe Ile Thr Leu Val Asn	
60 65 70	
GTA TTC ATT GST CAA GCT GAA CTA GCA GAA ATT CCA GAA GGC TAT GTC	340
Val Phe Ile Gly Gln Ala Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val	
75 80 85	
CCA GAA CAC TGG GAA TAT TAT AAG CAT CCC ATA TCA AGA TGG ATT GCC	388
Pro Glu His Trp Glu Tyr Tyr Lys His Pro Ile Ser Arg Trp Ile Ala	
90 95 100 103	
CGT AAT TTC TAT GAT AGT CCT GMA AAG ATA TAT GAA AGA ACA ATG	433
Arg Asn Phe Tyr Asp Ser Pro Xaa Lys Ile Tyr Glu Arg Thr Met	
110 115 120	

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..452
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..409
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..54
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 107..404
id AA038577

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..100
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 29..96
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 6..41
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..36
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..189
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 7..156
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 156..273
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 46..207
id H85485
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LDLLRGLPRVSLA/NL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

GAGACCAAGT GGCCTCCGAG CAGCTCAGGG CGCCCTTGAA AGTTCTTGA TCTGCGGGTT 60

ATG GCC GGT CCC TTG CAG GGC GGT GGG GCC CGG GCC CTG GAC CTA CTC 103
Met Ala Gly Pro Leu Gln Gly Gly Ala Arg Ala Leu Asp Leu Leu

-25	-20	-15	-10	
CGG GGC CTG CCG CGT GTG AGC CTG GCC AAC TTA AAG CCG AAT CCC GGC				156
Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly				
	-5	1	5	
TCC AAG AAA CCG GAG AGA AGA CCA AGA GGT CGG AAG AGA GGT AGA AAA				204
Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Gly Arg Lys				
	10	15	20	
TGT GGC AGA GGC CAT AAA GGA GAA AGG CAA AGA GGA ACC CGG CCC CGC				252
Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg				
	25	30	35	
TTG GGC TTT GAG GGA GGC CAG ACT CCA TTT TAC ATC CGA RTC CCA AAA				300
Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys				
	40	45	50	55
TAC GGG TTT AAC GAA GGA CAT AGT TTC AGA CGC CAG TAT AAG CCT TTG				348
Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu				
	60	65	70	
AGT CTC AAT AAG CTG CAG TAT CTT ATT GAT TTG GGT CGT GTT GAT CCT				396
Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro				
	75	80	85	
AGT CAA CCT ATT GAC TTA ACC CAG CTT GTC AAT GGG AGA GGT GTG ACC				444
Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr				
	90	95	100	
ATC GCG CCG				453
Ile Ala Pro				
	105			

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..103
id 711164
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 133..223
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 102..192
 id T11164
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..140
 (C) IDENTIFICATION METHOD: Von Haerje matrix
 (D) OTHER INFORMATION: score 4.1
 seq GILILWIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

AAAGGAAGCG GCTAACT ATG GCG ACC GCC ACG GAG CAG TGG GTT CTG GTG	50
Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val	
-40 -35	
GAG ATG GTA CAG GCG CTT TAC GAG GCT CCT GCT TAC CAT CTT ATT TTG	98
Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu	
-30 -25 -20 -15	
GAA GGG ATT CTG ATC CTC TGG ATA ATC AGA CTT CTT TTC TCT AAG ACT	146
Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr	
-10 -5 1	
TAC AAA TTA CAA GAA CGA TCT GAT CTT ACA GTC AAG GAA AAA GAA GAA	194
Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu	
5 10 15	
CTG ATT GAA GAG TGG CAA CCA GAA CCT CTT GTT CTT CTT GTC CCA AAA	242
Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys	
20 25 30	
GAC CAT CCT GGT CTC AAC TAC AAC ATC GTT TCA GGC CCT CCA AGC CAC	290
Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His	
35 40 45 50	
AAA ACT GTG GTG AAT GGA AAA GAA TGT ATA AAC TTC GCC TCA TTT AAT	338
Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn	
55 60 65	
TTT CTT GGA TTG TTG GAT AAC CCT AGG GTT AAG GCA GCA GCT TTA GCA	386
Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala	
70 75 80	
TCT CTA AAG AAG TAT GGC GTG GGG ACT TGT GGA CCC TGT	425
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys	
85 90 95	

(2) INFORMATION FOR SEQ ID NO: 256:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs
 (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 124..305
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..123
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..361
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..144
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 145..274
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 276..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 273..308
id H23328

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 147..309
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 146..308
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 69..145
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..40
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..36
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..182
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 222..258
id T62763
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..398
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq QGVLFICFTCAR/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AAAACTGAG GCCTGGGAGC AGGAACCTGT AGGCAGCGCT TGAGGGTAGC GGGATAGCAG 60
CTGCAACCGG CGTGGGAGGC GGGGGCTCTG GGCGGAACAA AAATCACAGG ATGTCAGAGG 120
ATGTTTCCCG GGAAGAACTG GGATAAAGGG GTCCCAGCAC C ATG GAG GAC CCG AAC 176
Met Glu Asp Pro Asn
-75
CCT GAA GAG AAC ATG AAG CAG CAG GAT TCA CCC AAG GAG AGA AGT CCC 224
Pro Glu Glu Asn Met Asa Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
-70 -65 -60
CAG AGC CCA GGA GGC AAC ATC TGC CAC CTG GGG GGC CCG AAG TGC ACC 272

Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr
-55 -50 -45

CGC TGC CTC ATC ACC TTC GCA GAT TCC AAG TTS SAG GAG CGT CAC ATG 320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa Xaa Glu Arg His Met
-40 -35 -30

AAG CGG GAG CAC CCA GCG GAC TTC GTG GCC CAG AAG CTG CAG GGG GTC 368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val
-25 -20 -15

CTC TTC ATC TGC TTC ACC TGC GCC CGC TCC TTC CCC TCT 407
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(166..452)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..302
id AA062591
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..45
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 43..89
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..45
id AA158431
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 444..490
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 43..89
id AA158431
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..160
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

AAGGATCCTC TACCGGCTTT TCGAGTCAGT GCTGCCGCCG CTGCCCGCGG CTTTGCAGAG 60
CAGG ATG AAT GTG ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG 109
Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu
-30 -25 -20
CAC TCC AAC GTG CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT 157
His Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn
-15 -10 -5
AAC AAC CCT GAG TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG 205
Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val
1 5 10 15
TAT CAT GCA GAT TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG 253
Tyr His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val
20 25 30
AGT AAG TAT ACC ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT AAA ACT 301
Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr
35 40 45
TCA AAA GTG AGA CCT TCA ACT GGA AAT TCT GCA TCT ACT CCA CAA AGT 349
Ser Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser
50 55 60
CAG TGT CTT CCA TCT GAA ATT GAA GTG AAA TAC AAA ATG GCT GAA TGT 397
Gln Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys
65 70 75
TAT ACA ATG CTA AAA CAA GAT AAA GAT GCC ATT GCT ATA CTT GAT GGG 445
Tyr Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly
80 85 90 95
KST CCC TTC AAG ACA AAG AAC TCC CAR AAT AAA CAT GAT GCT GGC 490
Xaa Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..312
id HSC26F061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 20..260
id W30546
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 66..252
id H34739
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AGGGTGCTGC CWKCCGGGTG CTGWTGCGAG TCGGTGGCAG CGAGGACATT TTCTGACTCC 60
CTGGCCCCCTG ACACGGGTGC ACTTTCATC CCGTCGCGGG GCCGGCCGCT ACTCCGGCCC 120
CAGG ATG CAG AAT GTG ATT AAT ACT GTG AAG GGA AAG GCA CTG GAA GTG 169
Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val
```

	-55	-50	-45	
GCT GAG TAC CTG ACC CCG GTC CTC AAG GAA TCA AAG TTT AAG GAA ACA				217
Ala Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr				
	-40	-35	-30	
GGT GTA ATT ACC CCA GAA GAG TTT GTG GCA GCT GGA GAT CAC CTA GTC				265
Gly Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val				
	-25	-20	-15	
CAC CAC TGT CCA ACA TGG CAA TGG GCT ACA GGG GAA GAA TTG AAA GTG				313
His His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val				
	-10	-5	1	5
AAG GCA TAC CTA CCA ACA GGC AAA TGG				340
Lys Ala Tyr Leu Pro Thr Gly Lys Trp				
	10			

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 89..262
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..423
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 334..402
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 260..321
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 428..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 401..438
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 62..295
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..43
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 401..444
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 312..345
id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 283..313
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 102..264
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 336..441
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 262..323
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 28..79
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 78..254
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 252..313
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..69
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..378
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 209..472
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq CIQRLPWLLLRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```
AGATCCCGCC TGGGGCCGSC TGAGTGGCAC TTAAGCGGGC CATGCCATGC AACCTTGGSC   60
GCTGCCAACC GTGGGCGAGC TCTGGGTGTG CGGGCGGCCT GCGCGGGCGC TCCGCTGTGT   120
CAGCGTGTTA TGATGCCGTC CCGTACCAAC CTGGCTACTG GAATCCCCAG TAGTAAAGTG   180
AAATATTCAA GGCTCTCCAG CACAGACG ATG GCT ACA TTG ACC TTC AGT TTA           232
                               Met Ala Thr Leu Thr Phe Ser Leu
                               -85
AGA AAA CCC CTC CAA AGA TCC CTT ATA AGG CCA TCG CAC TTG CCA CTG       280
Arg Lys Pro Leu Gln Arg Ser Leu Ile Arg Pro Ser His Leu Pro Leu
-80                               -75                               -65
TGC TGT TTT GAT TGG CGC CTT TCT CAT TAT TAT AGG CTC CCT CCT GCT       328
Cys Cys Phe Asp Trp Arg Leu Ser His Tyr Tyr Arg Leu Pro Pro Ala
-60                               -55                               -50
GTC AGG CTA CAT CAG CAA AGG GGG GGC AGA CCG GGC CGT TCC AGT GCT       376
Val Arg Leu His Gln Gln Arg Gly Gly Arg Pro Gly Arg Ser Ser Ala
```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 232..339
(C) IDENTIFICATION METHOD: blastp

- (D) OTHER INFORMATION: identity 97
region 143..250
id R57473
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 140..243
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 195..298
id H79944
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 243..279
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 299..335
id H79944
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 140..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 97..194
id H70394
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 235..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 193..363
id H70394
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 140..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 80..265
id W31972
est
- (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 123..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq PSLAAGLLFGSXK/GL
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AAATCGGGTT TCCGGAGAGA CCGGCTGCT GTGTCCCGCG GCTTGGCGCT CGTAGTGGAC 60

```

TCCGCGGGCC TTCGGCAGAT GCAGGCCTGG GGTAGTCTCC TTTCTGGACT GAGAAGAGAA 120
GA ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC 167
  Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
      -45                      -40          -35
TTT GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA 215
Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
      -30                      -25          -20
AAA ACA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTC GGC AGT 263
Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
      -15                      -10          -5
VWA GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCA AGR AAC GTT 311
Xaa Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
      1                      5          10
TGG GGT TTC CTA GCC GCT ACA TCT GTT
Trp Gly Phe Leu Ala Ala Thr Ser Val 338
  15                      20

```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..238
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..89
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 162..298
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 116..252
id T79527
est

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..56
id T79527
est

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 61..98
id T79527
est

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 59..159
id R08734
est

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 194..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 159..206
id R08734
est

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 14..56
id R08734
est

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 32..228
id H35655
est

(1X) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 108..304
id AA038389
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 108..161
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
AGGGGGTTGC GTCGCTCTCT GGTAAAGGCG TGCAGGTGTT GGCCGCGGCC TGTGAGCTGG    60
GATGAGCCGT GCTCCCGGTG GAAGCAAGGG GAGCCCCAGC SGGAGCC ATG GCC AGT    116
                                     Met Ala Ser
ACA GTG GTA GCA GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC    164
Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly
-15                      -10                      -5                      1
CGT TAC GTT TTG CAA GCC ATG AAG CAT ATG GAG CBT CAA GTA AAA CAA    212
Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln Val Lys Gln
                        5                      10                      15
GTT TTT CAA AGC CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA    260
Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg
                20                      25                      30
GGT EGG TTT GAA CCC ARA ATG RCA AAA CGG GAA GCA GCG GCG    302
Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala Gly
                35                      40                      45
```

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(B) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 96..277
id T32007

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..98
id T32007
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R59039
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 19..78
id R59039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 70..254
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..72
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 136..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```
AAAGTTCTCC TTCCACCTTC CCCCACCCTT CTCTGCCAAC CGCTGTTTCA GCCCCTAGCT    60
GGATTCACGC CATTGCTGCA GGTGCTCCAC AGCCCTTTTC AGGACCCAAA CACCCGCAGC    120
CGCTGTTCCT CAGGR ATG GTG ATC CGT GTA TAT ATT GCA TCT TCC TCT GGC    171
      Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
                        -80                        -75

TCT ACA GCG ATT AAG AAG AAA CAA CAA GAT GTG CTT GGT TTC CTA GAA    219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
      -70                        -65                        -60

GCC AAC AAA ATA GGA TTT GAA GAA AAA GAT ATT GCA GCC AAT GAA GAG    267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
      -55                        -50                        -45                        -40

AAT CGG AAG TGG ATG AGA GAA AAT GTA CCT GAA AAT AGT CGA CCA GCG    315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
                        -35                        -30                        -25

GIT CAG GGG CCA CAT GCT TTT CGG TAT AAA GCA TTC TCC TTC TCT AGG    363
Val Gln Gly Pro His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg
      -20                        -15                        -10

TTG CTA TCA CAG TGC AGA CCT GAC TGC CTG AAT ATG CTC AGG AGA TTT    411
Leu Leu Ser Gln Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe
      -5                        1                        5

AGT CAA TAT TGT CTG TAT TTG GTT ATG GAA AAG GCT CTC CTT TTT TTT    459
```

Ser Gln Tyr Cys Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe
10 15 20 25

TTT TTT
Phe Phe

465

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 117..274
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..116
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..355
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 270..302
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..330

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 113..311
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 36..112
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..41
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..330
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 94..292
id R25047
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 17..93
id R25047
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..352
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 38..331
id R23993
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 163..294
id W23811
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..194
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 131..193
id W23811
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..354
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 308..357
id W23811
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 350..390
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 354..394
id W23811
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 243..368
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq ITSSLFLGRGSA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```
AAGAAGCCGG TGGCCGCGCA GGAGGACGGA GCCCTAACCG CAACCCGCGC CGCGCCGCGC   60
CGATTTGATT TGTATCCACT GTCACCAGCA CTGCTCACTT AGGACTTTCT GGATCCAGAC  120
CCAGGCAGCG CACACTGGAC TCTTGAGGAA GAAGGAGACT CTAATTTTGG ATTCTTGGT   180
GGAGGAAAAT AAAACACTCT GGTCTGCCG CCAACGATGC AAGTGTGACT GCTGGCGTCT  240
TC ATG AGC TCC AGA GGT CAC AGC ACG CTA CCA AGG ACT CTC ATG GCC   287
  Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala
    -40                -35                -30

CCT CGG ATG ATT TCC GAG GGA GAC ATA GGA GGC ATT GGT CAA ATC ACC   335
Pro Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr
    -25                -20                -15

TCC TCT CTA TTC CTG GGC AGA GGC AGT GTG GCC TCC AAT CGG CAC CTC   393
Ser Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu
    -10                -5                1                5

CTC CAG GCT GGT GGC ATC                                           401
Leu Gln Ala Arg Gly Ile
    10
```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..183
id AA022583
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(69..228)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 281..440
id AA022584
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 66..119
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq PALCLFDVGGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```

AGGAAGTTCC GGGCCGAGTT CCTCGTGCCA ACGTGTCTTG TAAGGTGCGG CTAGAAACTG   60
GGGAC ATG GCA GCG CCT GGC CCA GCG CTC TGC CTC TTC GAC GTG GAT GGG   110
Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly
      -15                      -10                      -5

ACC CTC ACC GCC CCG CGG CAG AAA ATT ACC AAA GAA ATG GAT GAC TTC   158
Thr Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe
      1                      5                      10

CTA CAA AAA TTG AGG CAG AAG ATC AAA ATC GGA GTG GTA GGC GGA TCG   206
Leu Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser
      15                      20                      25

GAC TTT GAG AAA GTG CAG GAA CGG                               230
Asp Phe Glu Lys Val Gln Glu Arg
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 159..278
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 107..160
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 166..250
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 114..167
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 143..201
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..51
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 200..229
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 170..247
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 121..171
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 240..285
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..90
id N56221
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 126..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq ILFHSVVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
ACTGGAAGAA CTCGTCATGC TCTTTGTAGC GTGGTGCTTC TGTTGCTCAC AGGACAACTT   60
GCCTTTGATG ATTTTCAAGA GAGTTGTGCT ATGATGTGGC AAAGTATGCA GGAAGCAGGC   120
GGTCA ATG CCT CTG GGA GCA AGG ATC CTT TTC CAC GGT GTG TTC TAT GCC   170
      Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
                        -15                -10                -5

GGG GGC TTT GCC ATT GTG TAT TAC CTC ATT CAA AAG TTT CAT TCC AGG   218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
                1                5                10

ACA CTG   224
Thr Leu
```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..216
id HUM429E03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 235..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 211..303
id HUM429E03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 107..310
id T80259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 15..114
id T80259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..245
id T31768
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 271..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 234..290
id T31768
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 47..272
id N32697
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..43
id N32697
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..263
id N44613
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 156..194
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GCCTAGGTGT TGTCGTCCCT GCTAGTACTC CGGGCTGTGG GGGTCGGTGC GGATATTCAG   60
TCATGAAATC AGGGTAGGGA CTTCTCCCGC AGCGACGCGG CTGGCAAGAC TGTITGTGTT   120
GCGGGGGCCG GACTTCAAGG TGATTTTACA ACGAG ATG CTG CTC TCC ATA GGG       173
                               Met Leu Leu Ser Ile Gly
                               -10
ATG CTC ATG CTG TCA GCC ACA CAA GTC TAC ACC ATC TTG ACT GTC CAG       221
Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln
      -5                      1                      5
CTC TTT GCA TTC TTA AAC CTA CTG CCT GTA GAA GYA GAC ATT TTA GCA       269
Leu Phe Ala Phe Leu Asn Leu Leu Pro Val Glu Xaa Asp Ile Leu Ala
  10                      15                      20                      25
TAT AAC TTT GAA AAT GCA TCT CAG ACA TTT GAT GAC CTC CCT GCA AGA       317
Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Arg
                30                      35                      40
TTT GGT TAT                                                         326
Phe Gly Tyr

```

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..368
id AA150637
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 30..294
id H02763
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..372
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 148..339
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..147
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(267..394)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 231..358
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(184..277)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 349..442
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(109..164)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 464..519
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 72..250
id N30922
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..180
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..64
id N30922
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

AATCGCGGAG TCGGTGCTTT AGTACGCCGC TGGCACCTTT ACTCTGCCCG GCCGCGCGAA   60
CCCGTTTGAG CTCGGTATCC TAGTGCACAC GCCTTGCAAG CGACGGCGCC ATG AGT   116
                                         Met Ser
                                         -25

CTG ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC   164
Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
      -20                      -15                      -10

ATT GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT   212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
      -5                      1                      5

TAT GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG   260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
      10                      15                      20                      25

AAA GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTS RNA   308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Xaa Xaa
      30                      35                      40

GAT AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC   356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
      45                      50                      55

TGT GAT GGG GCT CAC ACA ARM VAT AAC GAA GAG ACT GGG CTG   398
Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
      60                      65                      70

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..150
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 31..126
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 151..212
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 126..187
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..35
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 211..242
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 185..216
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..263
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 202..410
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 172..206
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 159..230
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 174..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 279..340
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 129..163
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 189..299
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 298..338
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 159..193
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 201..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 337..371
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..252
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq YTAVSVLAGPRWA/DP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AATTACGCAG AGAGAAAGTT ACGAGAAACT CGTTTTTCATC TTCTGGTTT CATCYTAAAT   60
ACCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA GAA AAT TCT CAC AAT AAG   111
    Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys
        -60                -55                -50

GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA GTT GAA CGA AGC CAG GTT   159
Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val
    -45                -40                -35

CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG TGG CAA GAC TAT AAG CCT   207
Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro
    -30                -25                -20

GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT GGA CCC AGG TGG GCA GAT   255
Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp
    -15                -10                -5                1

CCT CAG ATC AGT GAV AGT VAT TTT TCT CCC AAG TTT AAC GAA AAG GAT   303
Pro Gln Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp
        5                10                15

GGG CAT GTT GAG AGA NAG AGC AAG AAT GGC CTG TAT GAG ATT GAN AAT   351
Gly His Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn
    20                25                30

GGA AGA CCG AGA AAT CCT GCA GAC GGA CTG GAC TGG TGG GGC   393
Gly Arg Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
    35                40                45

```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 137..335
id HSC1QH021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 126..263
id HUML12288
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..87
id HUML12288
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 178..443
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..266
id R60742
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..303
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 133..232
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 35..129
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..49
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..32
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 136..230
id C04685
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..147

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 10..132
id C04685
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 349..438
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

AAAACCTTAG CAAGATGGCG GCTCCCTGGG CGTCCCTGCG CCTGGTCGCC CCCATGTGGA 60
ATGGGCGTAT CAGGGGCATC CATCGCCTGG GTGCGGCAGT GGCCCCAGAG GGCAATCAGA 120
AGAAGAAAAG GACAATAMTC CARKTYCCTG GMCCVAASTA TTTCTACGAT GTGGAGGCTC 180
TGAGGGATTA CTTGCTCCAA AGGGAGATGT ACAAGGTGCA TGAGAAAAT CGATCTTACA 240
CCTGGCTGGA GAAGCAACAT GGTCCATACG GCGCAGGTGC CTTTTTCATC CTGAAGCAGG 300
GAGGCGCAGT CAAGTTTCGA GACAAGGAGT GGATCAGGCC AGATAAGT ATG GCC ATT 357
Met Ala Ile
-30
TCT CTC AGG AGT TCT GGA ATT TCT GTG AAG TGC CTG TCG AAG CTG TGG 405
Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser Lys Leu Trp
-25 -20 -15
ATG CGG TGG ACT GTG ACA TCA ACT ACG AGG GCC TGG ATM RNN GCN GAA 453
Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile Xaa Ala Glu
-10 -5 1 5
CCT CCG CAG CTG GAC ATC TCG 474
Pro Pro Gln Leu Asp Ile Ser
10

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..210

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 49..177
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..83
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 15..51
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 17..97
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FVLGSARLGGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```
AACATTAACC GGCAGG ATG TCG GAG GTG CGG CTG CCA CCG CTA CGC GCC CTG      52
      Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu
                -25                      -20

GAC GAC TTT GTT CTG GGG TCG GCG CGT CTT GGC GGC TCC GGA TCC ATG      100
Asp Asp Phe Val Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met
-15                -10                      -5                      1

CGA CCC GCT GCG ATG GTG YHA CCG CGT CAT CAA CAA CCT CCT CTA CTA      148
Arg Pro Ala Ala Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu
                5                      10                      15

CCA AAC CAA CTA CCT TCT CTG CTT CGG CAT CGG CCT CGC TCT CGC CGG      196
Pro Asn Gln Leu Pro Ser Leu Arg His Arg Pro Arg Ser Arg Arg
                20                      25                      30

GTA CGT ACG GCC ACG
Val Arg Thr Ala Thr
      35
```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 177..257
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 107..177
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 52..102
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 132..174
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id N44655
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 104..174
id N44655

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..170
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..226
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..40
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 63..169
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 169..249
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..39
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 206..250
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
AGGCGGCGAA GATGGCGGAG AACAGCGGTC GCGCCGGCAA GAGCAGCGGG AGCGNCGCGN 60
GGAAGGGGGC GGTGTCCGCA GAGCAGGTGA TTGCTGGCTT CAACCGCCTT CGGCAGGAAC 120
AGCGAGGCCT GGCATCCAAA GCAGCTGAGT TGGAGATGGA GTTGAATGAG CACAGCCTAG 180
TGAATCGATA CACTGAAGGA GGTAG ATG AAA CTC GTA AGT GCT ACC GCA TGG 232
                Met Lys Leu Val Ser Ala Thr Ala Trp
                -15                      -10

TTG GAG GAR TGC TGG TGG AGC GAA CTG TCA 262
Leu Glu Glu Cys Trp Trp Ser Glu Leu Ser
-5                      1
```

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 142..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 120..360
id HUML1108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 17..127
id HUML1108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 37..395
id AA156844
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 137..500
id HSU51712
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 112..270
id T70871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 9..111
id T70871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 105..213
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 206..315
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 314..347
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 309..410
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.3
seq LYVPLLAVCOLR3/77

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

AAGCTTCCAA ACCCAGGGCT TGCCTTGCC TTTGCCTCTT CCACCGCGCA GGGACCATGT   60
CGGCGGAGAC CGCGAGCGGC CCCACAGAGG ACCAGGTGGA AATCCTGGAG TACAACTTCA  120
ACAAGGTGCA CAAGCACCCG GATTCCACCA CGCTGTGCCT CATCGCGGCC GAGGCAGGCC  180
TTTCCGAGGA GGAGACCCAG AAATGGTTTA AGCAGCGCCT GGCAAAGTGG CGGCGCTCAG  240
AAGGCCTGCC CTCAGAGTGC AGATCCGTCA CAGACTAAGG AGATGGCAGG CATTGACAGC  300
TTCACCTCC ATG AAG GCC ATC TCT GTT TCT CTC CTC CGC TTA ACC AAG CTG   350
      Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu
                        -30                        -25

TTG TGG TTT TTC AGC ATA GTG TTG TAT GTT CCA TTG CTA GGT GTC TGC   398
Leu Trp Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys
-20                -15                -10                -5

TGT TTA CAC AGT GTT GTA TTT TTT                                     422
Cys Leu His Ser Val Val Phe Phe
                        1

```

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..421
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 179..405
id AA010936
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..91
id AA010936
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 108..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 91..188
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 443..505
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 429..491
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 417..449
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 402..434
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..187
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..494
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 300..478
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 195..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 178..313
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..513
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..445
id W44481
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..193
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 184..289
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 340..396
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 301..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 291..342
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 405..448
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 397..440
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..290
id W40172
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..439
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 343..441

id W40172
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 285..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 285..342
id W40172
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 85..438
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq LMIALTUVVGCIFM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

ACTCCAACGC TGGGTGACAT TGAGCTCACC AGCGCCACCG TCCCCGGGCGA AGTTCTGCGC   60
TGGTCGGCGCG AGTAGCAAGT GGCC ATG GGG AGC CTC AGC GGT CTG CGC CTG   111
      Met Gly Ser Leu Ser Gly Leu Arg Leu
      -115                               -110

GCA GCA GGA AGC TGT TTT AGG TTA TGT GAA AGA GAT GTT TCC TGN TCT   159
Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Xaa Ser
      -105                               -100                               -95

CTA AGG CTT ACC AGA AGC TCT GAT TTA AAG AGA ATA AAT GGA TTT TGC   207
Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys
      -90                               -85                               -80

ACA AAA CCA CAG GAA AGT CCC GGA GCT CCA TCC CGC ACT TAC AAC AGA   255
Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg
      -75                               -70                               -68

GTG CCT TTA CAC AAA CCT ACG GAT TGG CAG AAA AAG ATG CTC ATA TGG   303
Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp
      -60                               -55                               -50

TCA GGT CGC TTC AAA AAG GAA ANB NAA ATC CCA GAG ACT CTC TCG TTG   351
Ser Gly Arg Phe Lys Lys Glu Xaa Xaa Ile Pro Glu Thr Val Ser Leu
      -45                               -40                               -35                               -30

GAG ATG CTT GAN STT GCA AAG AAC AAG ATG CGA GTG AAG ATC AGC TAT   399
Glu Met Leu Xaa Xaa Ala Lys Asn Lys Met Arg Val Lys Ile Ser Tyr
      -25                               -20                               -15

CTA ATG ATT GCC CTG ACG GTG GTA GGA TGC ATC TTC ATG GTT ATT GAG   447
Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met Val Ile Glu
      -10                               -5                               1

GGC AAG AAG GCT GGC CAA AGA CAC GAG ACT TTA ACA AAG TTG AAC TTA   495
Gly Lys Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser Leu Xaa Leu
      5                               10                               15

GAA AAG AAA GCT CGT CTG   513

```

Glu Lys Lys Ala Arg Leu
20 25

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 190..399
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..141
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 139..198
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 139..311
id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..141

id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 144..300
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..95
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 93..152
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 122..338
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..73
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 71..137
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..360
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 121..283
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..72
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 346..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 270..326
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 70..129
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..358
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LASSFLFTMGSLG/PI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

ACTGTTTNGG	GGAGGCGCGT	GGGGCTTGAG	GCCGAGAACG	GGCCTTGCTG	CCACCAAC	58
ATG GAG ACT TTG TAC CGT GTC CCG TTC TTA GTG CTC GAA TGT CCC AAC	106					
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn						
-100 -95 -90 -85						
CTG AAG CTG AAG AAG CCG CCC TGG TTG CAC ATG CCG TCG GCC ATG ACT	154					
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr						
-80 -75 -70						
GTG TAT GCT CTG GTG GTG GTG TCT TAC TTC CTC ATC ACC GGA GGA ATA	202					
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile						
-65 -60 -55						
ATT TAT GAT GTT ATT GTT GAA CCT CCA AGT GTC GGT TCT ATG ACT GAT	250					
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp						
-50 -45 -40						
GAA CAT GCG CAT CAG AGG CCA GTA GCT TTC TTG GAT TAC AGA GTA AAT	298					

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 -35 -30 -25

GGA CAA TAT ATT ATG GAA GGA CTT GCA TCC AGC TTC CTA TTT ACA ATG 346
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Phe Leu Phe Thr Met
 -20 -15 -10 -5

GGA GGT TTA GGT TTC ATA ATC CTG GAC GGA TCG RNT GCA CCA AAT ATC 394
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile
 1 5 10

CCA AAA CTC AAT AGA TTC 412
 Pro Lys Leu Asn Arg Phe
 15

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
 region 80..132
 id C05215
 est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
 seq MLVLRSGLTAKALA/S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CACTCGGGAA GACTTCAGAG AAGTCTCACA AAGGACTCGG CTGGTGTGTT TTCTCAGTGC 60

CGAAGCCGCG CC ATG CTC GTT CTC AGA AGC GGC CTC ACC AAG GCG CTT GCC 111
 Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala
 -10 -5

TCA CGG ACC CTC GCG CTT CAG AKA AWT TTT GGT TTT CGA GCT GAA GTT 159
 Ser Arg Thr Leu Ala Xaa Gln Xaa Xaa Phe Ala Thr Arg Ala Glu Val
 1 5 10 15

CGG AAA GCG TTA GCG AAC TGT AAG GAA TGG CAA GAA GAA TGT ATC ATT 207

Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile
20 25 30

CCA AAT TTG GCT CGC ATT GAT AAA CAA GAG ACC AGG
Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Arg
35 40

243

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 77..206
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..77
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..194
id HUM427G10B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..65
id HUM427G10B
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 112..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 52..181
id R52722
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..52
id R52722
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 79..209
id W41484
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 30..137
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq NIESLAWTGGTLG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GAGTTTCCTG CGAGCTCGGC TTCCTCAAC ATG GCT GCG CCC TTG TCA GTG GAG	53
Met Ala Ala Pro Leu Ser Val Glu	
-35 -30	
GTG GAG TTC GGA GGT GGT GCG GAS TCC TGT TTG ACG GTA TTA AGA AAC	101
Val Glu Phe Gly Gly Gly Ala Xaa Ser Cys Leu Thr Val Leu Arg Asn	
-25 -20 -15	
ATC GAG TCA CTT GCC TGG ACA GGA GGA ACC CTG GGA CAT CCG GAA CCT	149
Ile Glu Ser Leu Ala Trp Thr Gly Gly Thr Leu Gly His Pro Glu Pro	
-10 -5 1	
GCT CAT CTG GAT CAA GAA GAA TTT GCT AAA AGA GCG GCC ASA GTT GTT	197
Ala His Leu Asp Gln Glu Glu Phe Ala Lys Arg Ala Ala Xaa Val Val	
5 10 15 20	
CAT CCA GGG AGA CAG CGT GCG GCC AGG AAT TCT GST GCT GAC TAC AGG	245
His Pro Gly Arg Gln Arg Ala Ala Arg Asn Ser Gly Ala Asp Tyr Arg	
25 30 35	

(2) INFORMATION FOR SEQ ID NO: 277:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..382
id AA127626
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 44..329
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 330..384
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..60
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..39
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 68..424
id N32938
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(56..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 67..414

id AA121528
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 164..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 130..344
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 36..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..130
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..392
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FVGGLP/VIEWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACTTAGTCGT GTGTACATCA TTGGGAATGG AGGGAAATAA ATGACTGGAT GGTGCTGCT 60
TTTTAAGTTT CAAATGACA TTCCAGACAA GCGGTGCCTG AGCCTGTGCC TGTCTTCAGA 120
TCTTCACAGC ACAGTTCCTG GGAAGGTGGA GCCACCAGCC TCTCCTTGAA TAACTGGGAG 180
ATGAPACAGG AAGCTCT ATG ACA CAC TTG ATC GAA TAT GAC AGA CAC CGA 230
          Met Thr His Leu Ile Glu Tyr Asp Arg His Arg
          -65                -60                -55
AAA TCA CGA CTC AGC CCC CTC CAG CAC CTC TAC CTG TTG CCC GCC GAT 278
Lys Ser Arg Leu Ser Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp
          -50                -45                -40
CAC AGC CGG AAT GCA GCT GAA AGA TTC CCT GGG GCC TGG TTC CAA CCG 326
His Ser Arg Asn Ala Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro
          -35                -30                -25
CCC ACT JTG GAC TCT GAG SCC TCT GCA TTT GTG GGT GGT CTG COT GTG 374
Pro Thr Val Asp Ser Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val
          -20                -15                -10
ATA TTT TGG TCA TGG GGT GGT CTG GTC 401
Ile Phe Trp Ser Trp Ala Gly Leu Val
          -5                1
```

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Uterus
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 70..337
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..268
 id HSC2SG081
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 71..251
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..181
 id R13964
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 256..334
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 184..262
 id R13964
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 26..255
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..230
 id H0ML13589
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 116..251
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..136
 id H05572
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 256..337
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 139..220
id H05572
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```
AACAGTTACG CGCCGCACGG ATC ATG GCC GCA GCC GCT CTG GGG CAG ATC TGG      53
                  Met Ala Ala Ala Ala Leu Gly Gln Ile Trp
                  -20                               -15

GCA CGA AAG CTT CTC TCT GTC CCT TGG CTT CTG TGT GGT CCC AGA AGA      101
Ala Arg Lys Leu Leu Ser Val Pro Trp Leu Leu Cys Gly Pro Arg Arg
          -10                               -5                               1

TAT GCC TCC TCC AGT TTC AAG GCT GCA GAC CTG CAG CTG GAA ATG ACA      149
Tyr Ala Ser Ser Ser Phe Lys Ala Ala Asp Leu Gln Leu Glu Met Thr
          5                               10                               15                               20

CAG AAG CCT CAT AAG AAG CCT GGC CCC GGC GAG CCC CTG GTG TTT GGG      197
Gln Lys Pro His Lys Lys Pro Gly Pro Gly Glu Pro Leu Val Phe Gly
                  25                               30                               35

AAG ACA TTT ACC GAC CAC ATG CTG ATG GTG GAA TGG AAT GAC AAG GGC      245
Lys Thr Phe Thr Asp His Met Leu Met Val Glu Trp Asn Asp Lys Gly
                  40                               45                               50

TGG GGC CAG CCC CGA ATC CAG CCC TTC CAG AAC CTC ACG CTG CAC CCA      293
Trp Gly Gln Pro Arg Ile Gln Pro Phe Gln Asn Leu Thr Leu His Pro
                  55                               60                               65

GCC TCC TCC AGC CTC CAC TAC TCC CTG CAG CTG TTT GAG GGC      335
Ala Ser Ser Ser Leu His Tyr Ser Leu Gln Leu Phe Glu Gly
          70                               75                               80
```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 50..169
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 219..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 213..338
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 2..336
id W79731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..326
id H21245
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 34..305
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 302..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 306..348
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 22..193
id W19567
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 201..284
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 183..266
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 283..344
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 266..327
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..161
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq CPLLLLVTNNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AAGGGGTGG AGGTCAGGGC GAGCGTCTCG CAGGCCGTAG GAGGAAG ATG GCG GTG      56
                                         Met Ala Val

GAG TCG CGC GTT ACC CAG GAG GAA ATT AAG AAG GAG CCA GAG AAA CCG      104
Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro Glu Lys Pro
-35              -30              -25              -20

ATC GAC CGC GAG AAG ACA TGC CCA CTG TTG CTA CTG GTC TTC ACC ACC      152
Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Leu Val Phe Thr Thr
              -15              -10              -5

AAT AAC GGC CGC CAC CAC CGA ATG GAG GAG TTC TCC CGG GGA AAT GTA      200
Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg Gly Asn Val
              1              5              10

CCG TCC AGC GAG TTG CAG ATC TAC ACT TGG ATG GAT GCA ACT TTG AAA      248
Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala Thr Leu Lys
              15              20              25

GAA CTG ACA AGC TTA GTA AAA GAA GTC TAC CCA GAA GCT AGA WAG AAG      296
Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala Arg Xaa Lys
              30              35              40              45

GGC ACT CAC TTC AAT TTT GCA VTC GTT TTT ACA GAT GTT AAA AGA CCT      344
Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val Lys Arg Pro
              50              55              60

```

(xi) INFORMATION FOR SEQ ID NO: 280:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 72..338
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 332..363
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..281
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 274..305
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 24..290
id H81957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: Blastn
- (D) OTHER INFORMATION: identity 92

region 59..324
id W82998
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 64..329
id AA023811
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 240..305
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPHTA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ACTAGCCTGC GAGTGTCTCTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA   60
GTAGTGAAAA CGTTGCTTCTT GAGGGGTGTC CAAGATGASC GGTTCAMCG GAGKTCAAGC  120
TGAACCAGCC ACCCGAGGAT GGCATCTCCT CCGTGAAGTT CAGCCCCAAC ACCTCCCACT  180
TCCTGCTTGT CTCCTCCTGG GACACGTCCG TCGTCTCTTA CGATGTGCCG GCCAACTCC   239
ATG CGG CTC AAG TAC CAG CAC ACC GGC GCC GTC CTG GAC TGC GCC TTC   287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
    -20                      -15                      -10

TAC GAT CCA ACG CAT GCC TGG AGT GGA GGA CTA GAT CAT CAA TTG AAA   335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
    -5                      1                      5                      10

ATG CAT GAT TTG AAC ACT GAT CAA GAA AAT CTT GTT GGG ACC ATG ATG   383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
          15                      20                      25

CCC CTA TCA GAT GTG TTG                                           401
Pro Leu Ser Asp Val Leu
          30
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 72..257
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 33..75
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..34
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 75..260
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..78
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 39..159
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92

region 144..223
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..42
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 84..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 55..166
id W71083
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ATAGGCGCAA G ATG GCG CTG CTT TTT GCA CGT TCT TTG CGC TTG TGC CGC	50
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg	
-85 -80 -75	
TGG GGA GCC AAA CGA TTG GGA GTT GCC TCC ACA GAG GCC CAG AGA GGC	98
Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly	
-70 -65 -60	
GTC AGT TTC AAA CTG GMA GAA AAA ACC GCC CAC AGC AGC CTG GCA CTC	146
Val Ser Phe Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu	
-55 -50 -45	
TTC AGA GAT GAT ACG GGT GTC AAA TAT GGC TTG GTG GGA TTG GAG CCC	194
Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro	
-40 -35 -30	
ACC AAG GTG GCC TTG AAT GTG GAG CGC TTC CGG GAG TGG GCA GTG GTG	242
Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val	
-25 -20 -15 -10	
CTG GCA GAC ACA GCG GTC ACC AGT GGC AGA GGG	275
Leu Ala Asp Thr Ala Val Thr Ser Gly Arg Gly	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 282:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE.
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 77..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```

ATTCCCCCTT GGGCGGTGGT GGAGGTGGTA ACCGTGATAG TAGCAGCTCC GCGGCAGCA    60
ACAGCGACTA CGAGGG ATG GCG GCG GCT GCA GCA GGA ACT SNA ACA TCC CAG    112
          Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln
                    -65                      -60

AGG TTT TTC CAG AGC TTC TCG GAT GCC CTA ATC GAC GAG GAC CCC CAG    160
Arg Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln
   -55                      -50                      -45

GCG GCG TTA GAG GAG CTG ACT AAG GCT TTG GAA CAG AAA CCA GAT GAT    208
Ala Ala Leu Glu Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp
   -40                      -35                      -30                      -25

GCA CAG TAT TAT TGT CAA AGA GCT TAT TGT CAC ATT CTT CTT GGG AAT    256
Ala Gln Tyr Tyr Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn
          -20                      -15                      -10

TAC TGT GTT GCT GTT GCT GAT GCA AAG AAG TCT CTA GAA CTC AAT CCA    304
Tyr Cys Val Ala Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro
          -5                      1                      5

AAT AAT TCC ACT GCT ATG CTG AGA AAA GGA ATA TGT GAA TAC CAT GAA    352
Asn Asn Ser Thr Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu
   10                      15                      20

AAA AAC TAT GCT GCT GCC CTA GAA ACT TTT TAC AGA AGG ACG GGG    397
Lys Asn Tyr Ala Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
   25                      30                      35

```

(12) INFORMATION FOR SEQ ID NO: 283:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 79..380
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..55
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 82..363
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..53
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 46..337
id R52491
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 65..247
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 2..53
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..52
 id R21494
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 266..305
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 268..307
 id R21494
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 129..321
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 71..263
 id AA084554
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 315..379
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 256..320
 id AA084554
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 139..318
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq WFIYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

AGTGGCCCGG ATGTTCGGTG CAGGTGCCAG ATCCGCTGAT CTAGTGCTTC TCGAAAAAAA   60
CCTTCAGGCG GCCCATGGCT GTCGATATTC AACCAGCATG CCTTGGACTT TATTSYGGGA   120
AGACCCOTATT ATTAAAAA ATG GGT CAA CTG AAA TAT ATG GAG AAT GTG GGG   171
          Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly
          -60                      -55                      -50
TAT GCG CAA GAG GAC AGA GAA CGA ATG CAC AGA AAT ATT GTC AGC CTT   219
Tyr Ala Gln Glu Asp Arg Gln Arg Met His Arg Asn Ile Val Ser Leu
          -45                      -40                      -35
GCA CAG AAT CTC CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG   267
Ala Gln Asn Leu Leu Asn Ile Met Ile Gly Ser Ile Leu Asp Leu Trp
          -30                      -25                      -20

```

CAA TGC TTC CTC TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG 315
Gln Cys Phe Leu Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg
-15 -10 -5

GGA AAA AGA GTT CCA GCG CAC TTT TCC AAC ACA TCA CTG CAT TAT TTG 363
Gly Lys Arg Val Pro Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu
1 5 10 15

AAT GCA GCA TGG CCG CGG 381
Asn Ala Ala Trp Pro Arg
20

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..292
id HUM524F05B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 43..176
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..279
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 16..50
id HS1799
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 57..181
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 175..234
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..45
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..51
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 101..228
id W81213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..107
id W81213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 8..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..165
id AA090080
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..210

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 159..202
id AA090080
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 174..266
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq WSPLSTRSGGTHA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

AAAAACAATA GGACGGAAAC GCCGAGGAAC CCGGCTGAGG CGGCAGAGCA TCCTGGCCAG 60
AACAGGCCAA GGAGCCAAGA CGAGAGGGAC ACACGGACAA ACAACAGACA GAAGACGTAC 120
TGGGGGCTGG ACTCCKCTGC CTCCCCCATC TCCCGCCCAT CTGCGCCCGG AGG ATG 176
Met
AGC CCA GGC TTC AGG GCC ATG GAT GTG GAG CCC CGC GCC AAA GGS TCC 224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30 -25 -20 -15
TTC TGG AGC CCT TTG TCC ACC AGG TCG GGG GGC ACT CAT GCG TGC TCC 272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
-10 -5 1
GCT TCA ATG AGA CAA CCC TGG 293
Ala Ser Met Arg Gln Pro Trp
5

(xii) INFORMATION FOR SEQ ID NO: 285:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..326
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 42..342
id R71425
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 11..337
id AA133412
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..345)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 172..403
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(71..114)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 402..445
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(26..76)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 439..489
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 186..359
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 83..182
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..76
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 33..86
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 39..345
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..307
 id R81019
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..179
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq SILAQVLDQSARA/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AGCGCTGACG CCGAGCC ATG GCG GAC GAG GAG CTT GAG GCG CTG AGG AGA      50
      Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg
                        -50                      -45

CAG AGG CTG GCC GAG CTG CAG GCC AAA CAC GGG GAT CCT GGT GAT GCG      93
Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala
      -40                      -35                      -30

GCC CAA CAG GAA GCA AAG CAC AGG GAA GCA GAA ATG AGA AAC AGT ATC      146
Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile
      -25                      -20                      -15

TTA GCC CAA GTT CTG GAT CAG TCG GCC CGG GCC AGG TTA AGT AAC TTA      194
Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu
      -10                      -5                      1                      5

GCA CTT GTA AAG CCT GAA AAA ACT AAA GCA GTA GAG AAT TAC CTT ATA      242
Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile
      10                      15                      20

CAG ATG GCA AGA TAT GGA CAA CTA AGT GAG AAG GTA TCA GAA CAA GGT      290
Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly
      25                      30                      35

TTA ATA GAR ATC CTT AAA AAA GTA AGC CAA CAA ACA GAA AAG AHN ACA      338
Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr
      40                      45                      50

ACA GTG AGG
Thr Val Arg
      55

```

(x) INFORMATION FOR SEQ ID NO: 286:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 186..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 156..352
id AA082259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 34..119
id AA082259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..33
id AA082259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 169..306
id H80945
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 30..122
id H80945
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 157..345
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq GLVCAGLADMARP/AE

(vii) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AACAGCGGGC AGGGAAAGCC GCGGGAAGGG TACTCCAGGC GAGAGGCGGA CGCGAGTCGT   60
CGTGGCAGGA AAAGTGA CTA GCTCCCCTTC GTTGT CAGCC AGGGACGAGA ACACAGCCAC   120
GCTCCCAMCC GGCTGCC HAA GRWTCCCTSG GCGGCG ATG TCG GCC GCC GGT GCC   174
                               Met Ser Ala Ala Gly Ala
                               -60
CGA GGC CTG CGG GCC ACC TAC CAC CGG CTC CTC GAT AAA GTG GAG CTG   222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
-55                               -50                               -45
ATG CTG CCC GAG AAA TTG AGG CCG TTG TAC AAC CAT CCA GCA GGT CCC   270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
-40                               -35                               -30
AGA ACA GTT TTC TTC TGG GCT CCA ATT ATG AAA TGG GGG TTG GTG TGT   318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25                               -20                               -15                               -10
GCT GGA TTG GCT GAT ATG GCC AGA CCT GCA GAA AAA CTT AGC ACA GCT   366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
-5                               1                               5
CAA TCT GVK GTT TTG ATG GCT ACA GGG TTT ATT TGG TCA AGA TAC TCG   414
Gln Ser Xaa Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10                               15                               20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 185..380
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 46..192
id W07314

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..478
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 401..470
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..390
id W07582
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..393
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 31..379
id W73850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..37
id W73850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..375
id AA112776
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..326
id H72671
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 98..355
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 287:

```

AACTTGTCAG CCCTTGCTCG AGGCGGAGGC AGCCCCGCGC CGCGCCGGAC CCGAGCATAT   60
TTCATTTTCT GTCATTGGAC TTTGAGCCAT TAGAACC ATG AGC AAC TAC AGT GTG   115
                               Met Ser Asn Tyr Ser Val
                               -85
TCA CTG GTT GGC CCA GCT CCT TGG GGT TTC CGG CTG CAG GGC GGT AAG   163
Ser Leu Val Gly Pro Ala Pro Trp Gly Phe Arg Leu Gln Gly Gly Lys
-80                               -75                               -70                               -65
GAT TTC AAC ATG CCT CTG ACA ATC TCT AGT CTA AAA GAT GGC GGC AAG   211
Asp Phe Asn Met Pro Leu Thr Ile Ser Ser Leu Lys Asp Gly Gly Lys
                               -60                               -55                               -50
GCA GCC CAG GCA AAT GTA AGA ATA GGC GAT GTG GTT CTC AGC ATT GAT   259
Ala Ala Gln Ala Asn Val Arg Ile Gly Asp Val Val Leu Ser Ile Asp
                               -45                               -40                               -35
GGA ATA AAT GCA CAA GGA ATG ACT CAT CTT GAA GCC CAG AAT AAG ATT   307
Gly Ile Asn Ala Gln Gly Met Thr His Leu Glu Ala Gln Asn Lys Ile
-30                               -25                               -20
AAG GGT TGT ACA GGA NYT TTG AAT ATG ACT CTG CAA AGA GCA TCT GCT   355
Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr Leu Gln Arg Ala Ser Ala
-15                               -10                               -5
GCA CCC AAG CCT GAG CCG GTT CCT GTT CAA AAG CCC ACA GTC ACC AGC   403
Ala Pro Lys Pro Glu Pro Val Pro Val Gln Lys Pro Thr Val Thr Ser
1                               5                               10                               15
GTG TGT TCC GAG ACT TCT CAG GAG CTA GCA GAG GGA CAG AGA AGA GGA   451
Val Cys Ser Glu Thr Ser Gln Glu Leu Ala Glu Gly Gln Arg Arg Gly
20                               25                               30
TCC CAG GGT GAC AGT AAA CAG CAA AAT   478
Ser Gln Gly Asp Ser Lys Gln Gln Asn
35                               40

```

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(iii) ORIGINAL SOURCE:

- (1) ORGANISM: Homo Sapiens
- (2) TISSUE TYPE: Uterus

(iv) FEATURE:

- (1) NAME/KEY: other

(B) LOCATION: 4..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..330
id N35568
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..297
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..272
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 295..338
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 271..314
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..212
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 209..313
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 13..320
id HSC1MA011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..339
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..278
id R61491
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 245..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEAG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

ATTCGTTTAC AGTTCGGCAC GTAGGACGGA GGGTAGTGCG TCTAGAGACA CATATTCCCA   60
ACGGATTGTA CGATGGTGTT CGGTCTTGAA TGGAAATGTA GTCTTAGGCC AGTCTTAGGT  120
TTTTGAACAG GATAGTAGGT ATCCGGAGTC GATTGAGGGC CAGAGCAGGC ACTGGGGTTC  180
GGATCCTGGG CAAAGTTTCC CACATTGAGG GTCTCGAGGA CGCCTAGATC TCTTTCCAG   240
GGCC ATG GCG AAC CCG AAG CTG CTG GGA CTG GAG CTA AGC GAG GCG GAG   289
      Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
          -15                -10                -5

GCG ATC GGT GCT GAT TCG GCG CGA TTT GAG GAG CTG CTG CTG CAG GCC   337
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
          1                5                10

TCG AAG GAG CTC CAG CAA                                           355
Ser Lys Glu Leu Gln Gln
      15

```

(x) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 90..178
id W21193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 2..53
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..89
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 269..345
id AA058174
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 204..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALLCTLLHFQNI/RR

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```
AAAGGTGTCT CGATCGGAGG GAGGTTCCGG TGGGCATCGG GCGGCTGGAA GAGCTCGACT   60
CGTCCCGCTG CGAAGCGCG AGTCTGAGTG GAACCCTGGA CGACTGCAG AGCGGCTGGC   120
CGACTCCTCT CGGACTACTG GAAGTCACAG CCAAAGAAAT TCTGTGATTA CTGCAAGTGC   180
TGGATAGCTT ACAATAGGCC TGT ATG ATA ATT CCG CTG TTA GAG ATT CTA ATA   233
          Met Ile Ile Pro Leu Leu Glu Ile Leu Ile
          -40                               -35
ATA ATT TTT AAT GAA GTG CTC CTT TTT GAT GTA AAC TCA GTT TAC   281
```

```

Ile Ile Val Leu Asn Glu Val Leu Leu Phe Asp Val Asn Ser Val Tyr
-30          -25          -20          -15

AAA GCA CTT TTA TGT ACA TTG CTC TTG CAT TTT CAA AAC ATC AGA AGA    329
Lys Ala Leu Leu Cys Thr Leu Leu Leu His Phe Gln Asn Ile Arg Arg
          -10          -5          1

TTT CTG TCT TCT CAG TCC CCT ATG AAA GCT GTG AGC CTT CTA THT TTT    377
Phe Leu Ser Ser Gln Ser Pro Met Lys Ala Val Ser Leu Leu Xaa Phe
          5          10          15

CAT CAA CCT GAC TTT GAT TAT ATA    401
His Gln Pro Asp Phe Asp Tyr Ile
      20          25

```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..382
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 97
region 4..337
id HUMGPCRB
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..54
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 345..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 55..92
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 30..235

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.4
 seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AACTTCAGTT TGGACAACCTA CTCACAGCTA CTACACAGAG ACCCGAACGA GTCAGTGATA    60
TACACCTGGA CCACCACCA ATG GAT ATA CAA ATG GCA AAC AAT TTT ACT CCG    112
      Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro
      -50                      -45

CCC TCT GCA ACT CCT CAG GGA AAT GAC TGT GAC CTC TAT GCA CAT CAC    160
Pro Ser Ala Thr Pro Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His
      -40                      -35                      -30

AGC ACG GCC AGG ATA GTA ATG CCT CTG CAT TAC AGC CTC GTC TTC ATC    208
Ser Thr Ala Arg Ile Val Met Pro Leu His Tyr Ser Leu Val Phe Ile
      -25                      -20                      -15                      -10

ATT GGG CTC GTG GGA AAC TTA CTA GCC TTG GTC GTC ATT GTT CAA AAC    256
Ile Gly Leu Val Gly Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn
      -5                      1                      5

AGG AAA AAA ATC AAC TCT ACC ACC CTC TAT TCA ACA AAT TTG GTT ATT    304
Arg Lys Lys Ile Asn Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile
      10                      15                      20

TCT GAT ATA CTT TTT ACC ACC GCT TTG CCT ACA CGA ATA GCT ACT ATG    352
Ser Asp Ile Leu Phe Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met
      25                      30                      35

CMA TGG GGY TTG ACT GGA GAA TCG GAG ATG TGG    385
Xaa Trp Ala Leu Thr Gly Glu Ser Glu Met Trp
      40                      45                      50
  
```

(2) INFORMATION FOR SEQ ID NO: 291:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: CDNA

(3) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (E) TISSUE TYPE: Pancreas

(4) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 55..462
 (C) IDENTIFICATION METHOD: fasta
 (D) OTHER INFORMATION: identity 99
 region 1..408
 id HUMORF06
 vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..218
id W77946
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 263..412
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 216..365
id W77946
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 412..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 366..416
id W77946
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..409
id C16991
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 263..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 212..411
id N28784
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 52..214
id N28784
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..58

id N28784
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..303
id C17735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 303..408
id C17735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 47..209
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 263..406
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 207..350
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 406..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..407
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..53
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 357..443
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AGTTCGTTTA TTCCTCCGCG CGCTGGGACA GGCTGCTTCT TCGCCAGAAC CAACCGGTTG    60
CTTGCTGTCC CAGCGGCGCC CCCTCATCAC CGTCGCCATG CCCGGAGGTC TGCTTCTCGG   120
GGACGTGGCT CCCAACTTTG AGGCCAATAC CACCGTCGGC CGCATCCGTT TCCACGACTT   180
TCTGGGAKAC TCATGGGGCA TTCTCTTCTC CCACCCTCGG GACTTTACCC CAGTGTGCAC   240
CACAGAGCTT GGCAGAGCTG CAAAGCTGGC ACCAGAATTT GCCAAGAGGA ATGTTAAGTT   300
GWTTCGCCCTT TCAATAGACA GTGTTGAGGA CCATCTTGCC TGGAGCAAGG ATATCA ATG   359
                                         Met
CTT ACA ATT GTG AAG AGC CCA CAG AAA AGT TAC CTT TTC CCA TCA TCG   407
Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser Ser
      -25                      -20                      -15

ATG ATA GGA ATC GGG AGC TTG CCA TCC TGT TGG GCA TGC TGG ATC CAG   455
Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile Gln
      -10                      -5                      1

CAG AGA
Gln Arg
      5
                                         461

```

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15
seq LFLLLLLAASAWG/VT

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```

Met Ser Ser Trp Ser Arg Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln
-35                      -30                      -25                      -20

Pro His Val Ser Arg Thr Leu Phe Leu Leu Leu Leu Leu Ala Ala Ser
      -15                      -10                      -5

```

Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser
 1 5 10
 Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly
 15 20 25
 Tyr Leu Pro Ala Thr
 30

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.2
seq LLLXAVLLSLASA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Xaa Ala Val Leu Leu
 -20 -15 -10
 Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 -5 1 5 10
 Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 15 20 25
 Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
 30 35 40
 Glu Ser Glu Leu Glu Xaa Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys
 45 50 55
 Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser
 60 65 70 75

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.1
seq CVLLLLLLLLLTRS/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
-20 -15 -10
Leu Leu Thr Arg Ser Ser Glu Val Glu Xaa Xaa Ala Glu Val Gly Gln
-5 1 5 10
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
15 20 25
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
30 35 40
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
45 50 55
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
60 65 70 75
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
80 85 90
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu
95 100

(x) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLFLFLAVDEAWA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala Val
-20 -15 -10
Asp Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Gly Arg
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq SLLLAVALGLATA/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Lys Ser Leu Ser Leu Leu Leu Ala Val Ala Leu Gly Leu Ala Thr
-15 -10 -5
Ala Val Ser Ala Gly Pro Ala Val Ile Glu Cys Trp Phe Val Glu Asp
1 5 10 15
Ala Ser Gly Lys Gly Leu Ala Lys Arg Pro Gly Ala Leu Leu Leu Arg
20 25 30
Gln Gly Pro Gly Glu Pro Pro Pro Arg Pro Asp Leu Asp Pro Glu Leu
35 40 45
Tyr Leu Ser Val His Asp Pro Ala Gly Ala Leu Gln Ala Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.6
seq LLTLXLLGGPTWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Leu Leu Leu Leu Thr Leu Xaa Leu Leu Gly Gly Pro Thr Trp Ala
-15 -10 -5
Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu
1 5 10 15
Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu
20 25 30
Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys
35 40 45
Leu Gly Ala Leu Xaa Gly Asn Thr Gln Glu Val Xaa Xaa Gln Pro Gly
50 55 60
Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly
65 70 75 80
Met Val Met Tyr Thr Ser Lys Asp Arg
85

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.4
seq LIILIXIWIWCLG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

Met Lys Ile Gly Ile Leu Leu Ser Leu Leu Asn Ser Val Ile Ser Gln
-45                -40                -35

Thr Leu Met Ser Cys Asn Trp Lys Gln Gln Met Arg Arg Met Lys Thr
-30                -25                -20                -15

Ile Leu Ile Ile Leu Ile Xaa Ile Trp Ile Trp Cys Leu Gly Ser Gln
                -10                -5                1

Thr Phe Gly Thr Ser Thr Thr Lys Ser Val Gln Leu Lys Ile Leu Arg
        5                10                15

Gln Asn Leu Ser His Phe Leu Gln Pro Pro Gln Val Ile
    20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.4
seq LPFLLSLFPGLP/VQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

Met Lys Ala Ser Ser Gly Arg Cys Gly Leu Val Arg Trp Leu Gln Val
-30                -25                -20                -15

Leu Leu Pro Phe Leu Leu Ser Leu Phe Pro Gly Ala Leu Pro Val Gln
                -10                -5                1

Ile Arg Tyr Ser Ile Pro Glu Glu Leu Ala Lys Asn Ser Val Val Gly
        5                10                15

Asn Leu Ala Lys Asp Leu Gly Leu Ser Val Arg Asp Leu Pro Ala Arg
    20                25                30

Lys Leu Arg Val Ser Ala Glu Lys Glu Tyr Phe Thr Val Asn Pro Glu
    35                40                45                50

Ser Gly Asp Leu Leu Val Ser Asp Arg Ile Asp Arg Asp Val
        55                60

```

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -33..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.1
 seq IIFLCHLLRGLHA/XT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ile Val Asp Cys Val Ser Ser His Leu Lys Lys Thr Gly Asp Gly
 -30 -25 -20

Ala Lys Thr Phe Ile Ile Phe Leu Cys His Leu Leu Arg Gly Leu His
 -15 -10 -5

Ala Xaa Thr Asp Arg Glu Lys Asp Pro Leu Met Cys Glu Asn Ile Gln
 1 5 10 15

Thr His Gly Arg Leu Pro
 20

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Ovary
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -104..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.1
 seq LTSLSWLLKASCS/KP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Ala Lys ... Leu Leu Phe Pro Ser Gly Arg Ser Val Arg Val Leu

Tyr Gly Ala Val Asn Lys Glu Arg Gln Xaa Glu Ser Val Leu Asn Arg
 -85 -80 -75
 Ala Cys Pro Pro Lys Ala Asn Ser Lys Glu Arg Arg Gly Arg Ala Val
 -70 -65 -60
 Leu Gly Ala Glu Leu Thr Gln Trp Ser Ser Pro Thr Thr Ala Gly Ser
 -55 -50 -45
 Cys Cys Ser Ser Cys Thr Leu Cys Ala Arg Ser Ser Ser Xaa Val Ile
 -40 -35 -30 -25
 Ala Pro Ser Pro Leu Val Pro Phe Thr Ser Gly Leu Thr Ser Leu Ser
 -20 -15 -10
 Trp Leu Leu Xaa Ala Ser Cys Ser Lys Pro Xaa Lys Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq LATKLLSLSGVFA/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
 -70 -65 -60
 Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
 -55 -50 -45
 Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala
 -40 -35 -30
 Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
 -25 -20 -15 -10
 Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
 -5 1 5
 Thr Ser Ala Val Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu

10 15 20
Ala Gly Met Pro Ser Pro Glu Trp Thr Xaa Arg Lys Lys Gln Thr Xaa
25 30 35
Glu Asn Trp Ala Trp Arg Asp Ser Arg Gln Arg Xaa Arg Gly Val Leu
40 45 50 55
Val Val Gly Ile Gly Ala
60

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VLWLISFFFTDGHG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
-15 -10 -5
Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
1 5 10 15
Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Met
20 25

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq WIFLAAILKGVQC/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```

Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
      -15                      -10                      -5
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
      1                      5                      10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
      15                      20                      25
Thr Asp Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      30                      35                      40                      45
Glu Trp Val Ala Asn Ile Xaa Ser Thr Ala Ser Gly Gly Thr Arg Gly
      50                      55                      60
Tyr Ala Ala Pro Val Lys Asp Arg Phe Ile Ile Ser Arg Asp Asp Ser
      65                      70                      75
Arg Asn Thr Leu His Leu Gln Met Asn Gly Leu Lys Xaa Met Thr Gln
      80                      85                      90
Ala Ile Tyr Tyr Cys Ala Thr
      95                      100

```

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LWRLLLWAGTAFQ/VX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

Met Ala Ala Pro Gly His Ser His His Leu Ser Ala Arg Val Arg Gly
      -37                      -30                      -25

```

```

Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala
-20          -15          -10

Gly Thr Ala Phe Gln Val Xaa Gln Gly Xaa Xaa Pro Glu Leu Xaa Ala
-5          1          5          10

Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr
15          20          25

Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Xaa Gly Leu Cys Thr
30          35          40

Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Xaa Xaa Ser Cys Asn
45          50          55

Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Xaa Pro Cys Ala
60          65          70          75

Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp
80          85          90

Glu Leu Pro His Gly Phe Ala Ala Ser Gln Pro Thr Trp Ser Trp Met
95          100          105

Thr Val Leu Leu Ser His
110

```

(2) INFORMATION FOR SEQ ID NO: 306:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(18) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq QACLLGLFALILS/GK

(19) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

Met Thr Ala Asp Pro Arg Lys Gly Arg Met Gly Leu Gln Ala Cys Leu
-25          -20          -15          -10

Leu Gly Leu Phe Ala Leu Ile Leu Ser Gly Lys Cys Ser Xaa Ser Pro
-5          1          5

Glu Pro Arg Gln Arg Arg Thr Leu Pro Pro Gly Trp Val Ser Leu Gly
15          20

```


Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln
 25 30 35
 Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro
 40 45 50 55
 Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp
 60 65 70
 Leu Val Arg Pro Ser Pro Leu Thr Pro
 75 80

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LCFLLAVAMSFF/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 -20 -15 -10
 Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
 -5 1 5
 Thr Arg Ala His Leu Leu Leu Lys Xaa Lys Met Met Arg Leu Gly Gly
 10 15 20
 Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
 25 30 35 40
 Thr Leu Xaa Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
 45 50 55
 Pro Pro Ser Met His Phe Phe
 60

(2) INFORMATION FOR SEQ ID NO: 308:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq LVLVLVVAVTVRA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```
Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg
   -15                -10                -5

Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val
   1                5                10                15

Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu
   20                25                30

Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His
   35                40                45

Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala
   50                55                60

Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr
   65                70                75

Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu
   80                85                90                95

Leu Leu Glu Leu Asp Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg
   100               105               110
```

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -102...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LXMTLMLPFKILS/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

```

Met Thr Ala Ala Ile Arg Arg Gln Arg Glu Leu Ser Ile Leu Pro Lys
  -100                               -95                               -90

Val Thr Leu Glu Ala Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg
  -85                               -80                               -75

Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro
  -70                               -65                               -60                               -55

Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu
  -50                               -45                               -40

Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile
  -35                               -30                               -25

Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Xaa Met Thr Leu Met Leu
  -20                               -15                               -10

Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg
  -5                               1                               5                               10

Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr
  15                               20                               25

Val Gly Glu Gly
  30
  
```

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Spleen

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -46...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq SIGVLTLSHLISG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Ser Ser Val Leu Ala Ala Ser His Pro Leu Val Leu Ser Ser Asn
  
```

```

-45          -40          -35
Ala Gly Thr Pro Gly Ile Ser Glu Lys Asp Asn Arg Asp Pro Ala Gly
-30          -25          -20          -15
Ser Ser Ile Gly Val Leu Thr Leu Ser His Leu Ile Ser Gly Leu Arg
          -10          -5          1
Thr Leu Tyr Thr Leu Leu His Phe Pro Leu Arg
          5          10

```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LIILGLVLFMVYG/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly
-5          -45          -40          -35
Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val
          -30          -25          -20
Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val
          -15          -10          -5
Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu
          1          5          10
Arg Arg Ala Glu Gly Leu Tyr Xaa Gln Leu Leu Gly Leu Thr Ala Ser
          15          20          25          30
Thr Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp
          35          40          45
Ala Ile Met Gln Met Trp Leu Asn Ala
          50          55

```

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SCLVSGWGLLANG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 -60 -55 -50

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 -45 -40 -35

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 -30 -25 -20

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 -15 -10 -5

Gln Arg
1

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VICCVLFLLFILG/YI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```

Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro
  -45                      -40                      -35

Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
  -30                      -25                      -20

Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr
  -15                      -10                      -5                      1

Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val
           5                      10                      15

Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn
      20                      25                      30

Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu
      35                      40                      45

Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr
      50                      55                      60                      65

Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Xaa Xaa
           70                      75                      80

Lys Thr Ser Ser His Arg Leu Leu Gly Lys Ser Ser Ile Gln
      85                      90                      95

```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLLFLAWVCFIFY/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe Leu
  -15                      -10                      -5

Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu Thr Arg
      1                      5                      10

Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro Gly Pro Gly
      15                      20                      25                      30

```

Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala Cys Trp Met Ala
 35 40 45

Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile Asp Ala Leu Arg Phe
 50 55 60

Asp Phe Ala Gln Pro Gln His Ser His Val Pro Arg Glu Pro Pro Val
 65 70 75

Ser Leu Pro Phe Leu Gly Lys Leu Ser Ser Leu Gln Arg Ile Leu Glu
 80 85 90

Ile Gln Pro His His Ala Arg Leu
 95 100

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq CWMMLLGSGSFL/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Ser Pro Val Leu His Phe Tyr Val Arg Pro Ser Gly His Glu Gly
 -80 -75 -70

Ala Ala Ser Gly His Thr Arg Arg Lys Leu Gln Gly Lys Leu Pro Glu
 -65 -60 -55 -50

Leu Gln Gly Val Glu Thr Glu Leu Cys Tyr Asn Val Asn Trp Thr Ala
 -45 -40 -35

Glu Ala Leu Pro Ser Ala Glu Glu Thr Lys Lys Leu Met Trp Leu Phe
 -30 -25 -20

Gly Cys Pro Tyr Cys Trp Met Met Leu Leu Gly Ser Xaa Gly Ser Phe
 -15 -10 -5

Leu Ala Pro Met Thr Cys Xaa Trp Arg Ser
 1 5

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq ILRLGSLSNAYS/PR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
-35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
-20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
 1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
15 20 25

Pro Ser Asn Met Tyr Thr Lys Tyr Tyr Ile His Arg Asn Gly
30 35 40

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq LLRVNLNLPNSIG/CV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Met Gly Val Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro
 -20 -15 -10

His Asn Ser Ile Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu
 -5 1 5 10

Glu Trp Leu Asn Leu Ala Gly Asn Asn Leu Lys Ala Met Glu Gln Xaa
 15 20 25

Asn Ser Cys Thr Ala Leu Gln His Leu Asp
 30 35

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq ILRLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
 -35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
 -20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
 1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
 15 20 25

Arg

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1
Ala Ala Ser Met Gln Glu Glu Val Arg Thr Ala Pro Arg Ala Leu
5 10 15

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -47..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq GCGMFTFLSSVXA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
-45 -40 -35
Gly Thr Ala Val Glu Thr Glu Gly Xaa Gly Ser Arg His Pro Pro Trp
-30 -25 -20
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Xaa Ala Ala
-15 -10 -5 1
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
5 10 15
Leu Leu Gln Ile Lys Thr Leu Leu Ala Xaa Ser Cys His Glu Gln Glu

20 25 30
Met Val Val Ser Ser Leu Val Ile Gly .
35 40

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.2
seq LLFPVGRSWSCFA/QT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Glu Thr Phe Leu Glu Pro Asn Asn Lys Lys Leu Leu Phe Pro Val
-20 -15 -10
Gly Arg Ser Trp Ser Cys Phe Ala Gln Thr Xaa Ser Leu Ala Lys Tyr
-5 1 5
Ile Pro Tyr Ser Leu Trp Lys Tyr Ser Val Leu Ser Gly His Ser
10 15 20

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -15..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.1
seq FLWGLALPLFFFC/WE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Gly Phe Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys Trp
-15          -10          -5          1
Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala
          5          10          15
Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu
          20          25          30
Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr
          35          40          45
Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Val Pro Glu Ala Glu Thr
          50          55          60          65
Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr
          70          75          80
Lys Thr Xaa Pro Asn Phe Met Val Leu Xaa Xaa Xaa Val Thr
          35          90          95

```

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLLSDILGQGATA/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

```

Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
-20          -15          -10
Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
-5          1          5          10
Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
          15          20          25
Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
          30          35          40

```

Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Gly
45 50 55

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ICAGSVLPPYSNC/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Val Glu Ile Cys Ala Gly Ser Val Leu Pro Pro Tyr Ser Asn Cys
-15 -10 -5

Gln Met Pro Glu Pro Ser Ile Phe Thr Leu Ile His Phe His Thr Tyr
1 5 10 15

Tyr Cys Leu Thr Thr Pro Gln
20

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LLAFGTSCSVVXY/XP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

```

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn
      -40                      -35                      -30

Arg Val Arg Gly Val Leu Asn Trp Xaa Ser Gly Pro Arg Gly Leu Leu
      -25                      -20                      -15

Ala Phe Gly Thr Ser Cys Ser Val Val Xaa Tyr Xaa Pro Leu Xaa Arg
      -10                      -5                      1                      5

Val Val Val Thr Xaa Leu Xaa Gly His Thr Ala Arg Val Asn Cys Ile
              10                      15                      20

Gln Trp Ile Xaa Lys Gln Xaa Gly Met
              25                      30

```

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq QLLLATLQEAATT/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
-70                      -65                      -60                      -55

Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
      -50                      -45                      -40

Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
      -35                      -30                      -25

Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Ala Thr Leu
      -20                      -15                      -10

Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
      -5                      1                      5                      10

Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
              15                      20                      25

Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
              30                      35                      40

```

Gln Leu Ser Pro Ser
45

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLPFGMLCASSTT/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro
-25 -20 -15
Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His
-10 -5 1 5
Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
10 15 20
Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
25 30 35
Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
40 45 50
Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu
55 60 65

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -110..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq HTXGLLGFRXQG/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

```

Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
-110                      -105                      -100                      -95

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
                      -90                      -85                      -80

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
                      -75                      -70                      -65

Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
                      -60                      -55                      -50

Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
-45                      -40                      -35

Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Xaa Ala Arg Arg Thr
-30                      -25                      -20                      -15

Leu His Thr Xaa Gly Leu Leu Gly Phe Gly Arg Xaa Gln Gly Ser Ile
                      -10                      -5                      1

Pro Lys Gly Pro Glu Gly Leu Xaa Asp Glu Phe Val Xaa Ser Ile Xaa
          5                      10                      15

Thr Trp Arg Glu Thr Trp
20

```

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Large intestine

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq PLSMILLSDKIQS/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Lys Val Thr Gly Ile Thr Ile Leu Phe Trp Pro Leu Ser Met Ile
 -20 -15 -10

Leu Leu Ser Asp Lys Ile Gln Ser Ser Lys Arg Glu Val Gln Cys Asn
 -5 1 5

Phe Thr Glu Lys Asn Tyr Thr Leu Ile Pro Ala Asp Ile Lys Lys Asp
 10 15 20

Val Thr Ile Leu Asp Leu Ser Tyr Asn Gln Xaa Thr Leu Asn Gly Thr
 25 30 35 40

Asp Thr

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq HLSWSSSAYQAWA/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Ala Ala Gly Arg Ala Gln Val Pro Ser Ser Glu Gln Ala Trp Leu
 -95 -90 -85

Glu Asp Ala Gln Val Phe Ile Gln Lys Thr Leu Cys Pro Ala Val Lys
 -80 -75 -70 -65

Glu Pro Asn Val Gln Leu Thr Pro Leu Val Ile Asp Cys Val Lys Thr
 -60 -55 -50

Val Trp Leu Ser Gln Gly Arg Asn Gln Gly Ser Thr Leu Pro Leu Ser
 -45 -40 -35

Tyr Ser Phe Val Ser Val Gln Asp Leu Lys Thr His Gln Arg Leu Pro
 -30 -25 -20

Cys Cys Ser His Leu Ser Trp Ser Ser Ser Ala Tyr Gln Ala Trp Ala
 -15 -10 -5

Gln Glu Ala Gly Pro Asn Gly Asn Pro Pro Gly
 1 5 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Ala Asp Glu Asp Leu Cys Tyr Cys Leu Gly
20 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

BNSDOCID: <WO__9906548A2_I_>

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LLXCVGNFFGSTQ/DA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Ala Gln Lys Pro Leu Arg Leu Leu Ala Cys Gly Asp Val Glu Gly
 -45 -40 -35

Lys Phe Asp Ile Leu Phe Asn Arg Val Gln Ala Ile Gln Lys Xaa Ser
 -30 -25 -20

Gly Asn Phe Asp Leu Leu Xaa Cys Val Gly Asn Phe Phe Gly Ser Thr
 -15 -10 -5

Gln Asp Ala Glu Trp Glu Glu Tyr Lys Thr Gly Ile Lys Lys Ala Pro
 1 5 10 15

Ile Gln Thr Tyr Val Leu Gly Ala Asn Asn Gln Glu Thr Val Lys Tyr
 20 25 30

Phe Gln Asp Ala Asp Gly Cys Glu Leu Ala Glu Asn Ile Thr Tyr Leu
 35 40 45

Gly Arg Gly
 50

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -52..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RPVLLHLHQTAAH/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
  -50                      -45                      -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
  -35                      -30                      -25

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
  -20                      -15                      -10                      -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
                      1                      5                      10

Gln Gln Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
  15                      20                      25

Ile Ala Xaa Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Xaa His
  30                      35                      40

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile
  45                      50                      55
  
```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -52..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RPVLLHLHQTAAH/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Xaa Trp Lys Met
  -50                      -45                      -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
  -35                      -30                      -25
  
```

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
 -20 -15 -10 -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
 1 5 10

Gln Gly

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser
 -35 -30 -25

Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala
 -20 -15 -10 -5

Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln
 1 5 10

Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro
 15 20 25

Gln Xaa Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val
 30 35 40

Glu Lys Asn Lys Tyr Asp Ala Thr Gly
 45 50

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -58..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LVSFVSSSEGTEQ/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Arg Asp Cys Pro Gly Val Glu Xaa Ile Leu Asp Cys Ser Xaa Arg
-55 -50 -45
Gln Lys Thr Glu Gly Cys Arg Leu Gln Ala Gly Lys Glu Cys Val Asp
-40 -35 -30
Ser Pro Val Glu Gly Gly Gln Ser Glu Ala Pro Pro Ser Leu Val Ser
-25 -20 -15
Phe Ala Val Ser Ser Glu Gly Thr Glu Gln Gly Glu Asp Pro Arg Ser
-10 -5 1 5
Glu Lys Asp His Ser Arg Pro His Lys His Arg Ala Arg His Ala Arg
10 15 20
Leu Arg Arg Ser Glu Ser Leu Ser Xaa Lys Gln Val Lys Glu Ala Lys
25 30 35
Ser Xaa Cys Lys Ser Ile Ala Leu Leu Leu Thr Asp Ala Pro Xaa Pro
40 45 50
Asn Ser Lys Gly Val Leu Met Phe Lys Lys Arg
55 60 65

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -37..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LVFNELLILT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
  -35                      -30                      -25
Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
  -20                      -15                      -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
  -5                      1                      5                      10
Leu His Glu Thr Gly Gly Ala Met Val Tyr
          15                      20

```

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4
seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
  -25                      -20                      -15
Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
  -10                      -5                      1
Val Leu Xaa Xaa Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala
  5                      10                      15
Asp Leu
  20

```

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.6
seq LLALLTVSTPSWC/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe Leu
-30 -25 -20
Leu Ser Ser Leu Leu Ala Leu Thr Val Ser Thr Pro Ser Trp Cys
-15 -10 -5
Gln Ser Thr Glu Ala Ser Pro Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.8
seq SLLLLLLKCVHWS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Glu Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Leu Leu
-25 -20 -15
Leu Leu Leu Leu Xaa Cys Val His Trp Ser Gln Pro Ser Leu Leu Ser
-10 -5 1 5
Trp

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYLEA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20 -15 -10 -5
Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
1 5 10
Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
15 20 25
Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
30 35 40
Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
45 50 55 60
Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
65 70 75
Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
80 85 90
Thr Thr Asp Lys
95

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -46..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.3
seq LVLLLVLTLCSL/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala
-45 -40 -35
Val Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly
-30 -25 -20 -15
Ala Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro
-10 -5 1
Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser
5 10 15
Arg Gln Lys Ala Leu Ser Pro Lys
20 25

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.1
seq LLLQLAWLGAALA/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Ala Pro Leu Leu Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala
-15 -10 -5
Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr
1 5 10 15
Lys Met Pro Ala Leu His Arg His Glu Glu Glu Lys Phe Phe Leu Asn
20 25 30
Ala Lys Gly Gln Lys Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr
35 40 45

Lys Gln Leu Ser Val Val Val Pro Ser Tyr Asn Glu Glu Lys Arg Leu
 50 55 60

Pro Val Met Met Asp Glu Ala Leu Ser Tyr Leu Glu Lys Arg Gln Lys
 65 70 75 80

Arg Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser
 85 90 95

Lys Asp Gln Thr Ser Lys
 100

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.8
seq SALLVGFLSVIFA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Xaa Leu Leu Gly Ser Ala
 -25 -20 -15

Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu
 -10 -5 1 5

His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn
 10 15 20

Trp Xaa Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile
 25 30 35

Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu
 40 45 50

Leu Met Lys Ser Ile His Ala Xaa Leu Asn Ala Val Ala Ala Ile Leu
 55 60 65

Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn
 70 75 80 85

Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala
 90 95 100

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq LALSLLILVLAFG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
   -15                      -10                      -5

Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
   1                      5                      10          15

Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
          20                      25                      30

Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
          35                      40                      45

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
          50                      55                      60

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
          65                      70                      75

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
          80                      85                      90          95

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
          100                     105                     110

Gln

```

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(3) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.4
seq AMWLLCVALAVLA/WG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1

Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15

Gln Gly Asa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30

His Pro Asp Asp Glu Ala Met Trp
35 40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(3) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(3) LOCATION: -38..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8
seq LVFTVSLFAWICC/QR

(K1) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

```
Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
      -35                      -30                      -25

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
      -20                      -15                      -10

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
      -5                      1                      5                      10
```

Pro Pro Tyr Lys Phe Val His Val Leu Xaa Gly Val Asp Ile Tyr Pro
 15 20 25

Glu Asn Leu Asn Ser Lys Lys Lys
 30

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
 seq GWLVLCVLAISLA/SM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
 -15 -10 -5

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
 1 5 10

Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys
 15 20 25 30

Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln
 35 40 45

Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly
 50 55 60

Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile
 65 70 75

Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln
 80 85 90

Pro Arg Pro Ala Phe Ser Ala Ile Arg
 95 100

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -63..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.2
seq VLLTLLLI AFIL/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Thr Ala Trp Glu Ala Met Ala Pro His Val Asn Pro Thr Leu Lys
-60 -55 -50
Asp Lys Ala Leu Ser Pro Gln Gln Xaa Xaa Xaa Thr Ser Pro Ala Pro
-45 -40 -35
Cys Xaa Ser Asn His His Asn Lys Lys His Leu Ile Leu Ala Phe Cys
-30 -25 -20
Ala Gly Val Leu Leu Thr Leu Leu Leu Ile Ala Phe Ile Phe Leu Ile
-15 -10 -5 1
Ile Lys Ser Tyr Arg Lys Tyr His Ser Lys Pro Gln Ala Pro Gly
5 10 15

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LLCECLLLXAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:


```

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Xaa Ala Gly
      -15                -10                -5

Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
      1                5                10

Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala Lys Tyr Gly Ile
      15                20                25                30

Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys Ala Xaa Glu Ile
      35                40                45

Ser Glu

```

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LVXSLPVMHCLTFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met Gly His Ala Met Gly Leu Val Xaa Ser Leu Pro Val His Cys Leu
      -15                -10                -5

Thr Phe Ala Ser Ser Ala Pro Ser Ser Pro Gln Pro Thr Arg Met Trp
      1                5                10

Phe Xaa Ala Gln Ala His Xaa Pro Pro Leu Ile Leu Gly Pro
      15                20                25

```

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
-15 -10 -5
Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
1 5 10 15
Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
20 25 30
Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
35 40 45
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
50 55 60
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
65 70 75 80
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
85 90 95
Val Leu Ile Trp
100

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -59..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq VLAQLAFLSQISQ/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser
 -55 -50 -45
 Ile His Arg Gln His Ser Lys Asp Leu Gln Asp Ile Val Ala Thr Leu
 -40 -35 -30
 Gly Pro Arg Ser Ala Thr His Pro His Gln Pro Ala Ile Gln Val Leu
 -25 -20 -15
 Ala Gln Leu Ala Phe Leu Ser Gln Ile Ser Gln Cys Ile Ile Ser Gln
 -10 -5 1 5
 Arg

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15
 Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1
 Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 5 10 15 20
 Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly Val Ile Ser Gly Ala
 25 30 35
 Val Phe Leu Ile Ile Leu Phe Cys
 40

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Phe Lys Val Ile Gln Arg Ser Val Gly Pro Ala Ser Leu Ser Leu
-20 -15 -10
Leu Thr Phe Lys Val Tyr Ala Ala Pro Lys Lys Asp Ser Pro Pro Lys
-5 1 5
Asn Ser Val Lys Val Asp Glu Leu Ser Leu Tyr Ser Val Pro Glu Gly
10 15 20 25
Gln Ser Lys Tyr Val Glu Glu Ala Arg Ser Gln Leu Glu Glu Ser Ile
30 35 40
Ser Gln Leu Arg His Tyr Cys Glu Pro Tyr Thr Thr Trp Cys Gln Glu
45 50 55
Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -136..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu Ser Gly Arg Thr Lys
  -135                      -130                      -125

Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser Thr Ser His Gly Phe
-120                      -115                      -110                      -105

Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln Phe Pro Gly Gly Ser
                      -100                      -95                      -90

Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly Ile Leu Thr Leu Asn
      -85                      -80                      -75

Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val Met Met Leu Gln Leu
      -70                      -65                      -60

Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr Glu Gly Lys Gly Leu
      -55                      -50                      -45

Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser Gly Ser Asp Leu Asn
-40                      -35                      -30                      -25

Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro Leu Ile Ser Val Ala
      -20                      -15                      -10

Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala Ala
      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq PLLKILHAAGAQG/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser Asp Ser Ala
      -40                      -35                      -30

Cys Arg Ile Ser Pro Gly Gln Ile Asn Xaa Val Arg Pro Lys Leu Pro
      -25                      -20                      -15

Leu Leu Lys Ile Leu His Ala Ala Gly Ala Gln Gly Glu Met Phe Thr

```

-10

-5

1

Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met Val Lys Gln
 5 10 15 20

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq AFAWLGVVPLTAC/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu Gly
 -110 -105 -100

Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser Ile
 -95 -90 -85

Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser Arg
 -80 -75 -70 -65

Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro Ile
 -60 -55 -50

Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe Ala
 -45 -40 -35

Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His Tyr
 -30 -25 -20

Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala Cys
 -15 -10 -5

Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu Thr
 1 5 10 15

Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys Leu
 20 25 30

Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 361:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
 seq MLIMLGIFENVHS/AV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu  
-10 -5 1

Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Xaa Gly Pro Gln  
5 10 15

Asn Ile Tyr Asn Leu Tyr Glu His Gly  
20 25

(2) INFORMATION FOR SEQ ID NO: 362:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(71) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(1X) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -112..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
                        seq AAVAVGMLXASYA/AV
```

42) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Gly Leu Trp Arg Pro Gly Trp Arg Cys Val Pro Phe Cys Gly
-110 -105 -100

```

Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu Arg Val
-95                      -90                      -85

Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala Glu Arg
-80                      -75                      -70                      -65

Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg Ala Arg
-60                      -55                      -50

His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn Pro Phe
-45                      -40                      -35

Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr Thr Leu
-30                      -25                      -20

Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser Tyr Ala
-15                      -10                      -5

Ala Val
1

```

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (C) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SDPLCVLFLNTSG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val Ser Cys Ala
-35                      -30                      -25

Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro Leu Cys Val
-20                      -15                      -10

Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val Glu Arg Thr
-5                      1                      5

Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys Thr Phe Ile
10                      15                      20                      25

Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe Gly Val Tyr
30                      35                      40

```


Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp Phe Leu Gly
 45 50 55

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPHTA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly
 -70 -65 -60 -55
 Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val
 -50 -45 -40
 Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
 -35 -30 -25
 Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10
 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Xaa Xaa Lys
 -5 1 5 10
 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp
 15 20 25
 Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Ser
 30 35

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq AHLWCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

```
Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys
-25                -20                -15                -10

Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
          -5                      1                      5

Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp
      10                15                20
```

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq MLAVSLTVXLLGA/MM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```
Met Leu Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu
      -10                -5                1

Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
      5                10                15

Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
      20                25                30                35

Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
      40                45                50
```

Gly Asp Val Met Phe Thr Gly Ser Trp
55 60

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -76..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq MLELDLLVFHLWG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Ser Ser Thr Leu Ala Lys Ile Ala Glu Ile Glu Ala Glu Met Ala
-75 -70 -65

Arg Thr Gln Lys Asn Lys Ala Thr Ala His His Leu Gly Leu Leu Lys
-60 -55 -50 -45

Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu Ile Thr Pro Lys Gly Gly
-40 -35 -30

Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp Trp Pro Arg Gln Val Met
-25 -20 -15

Leu Glu Leu Asp Leu Leu Val Phe His Leu Trp Gly Ser Gln His Cys
-10 -5 1

Leu Val Thr Trp Gln Gly
5 10

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -45..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.9
 seq LVLALLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45                -40                -35                -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
                -25                -20                -15

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val
                -10                -5                1

Ser Arg Thr Asp Ser Pro Ser Pro Leu
    5                10
  
```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -25..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.9
 seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
-25                -20                -15                -10

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
                -5                1                5

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
    10                15                20

Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
    25                30                35
  
```

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```

Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
      -85                      -80                      -75

Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
      -70                      -65                      -60

Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
      -55                      -50                      -45

Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
      -40                      -35                      -30                      -25

Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
      -20                      -15                      -10

Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
      -5                      1                      5

Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
      10                      15                      20

Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
      25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6
seq VFCLLAVAPGAHS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
 -15 -10 -5

Ala His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys
 1 5 10

Pro Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe
 15 20 25

Thr Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu
 30 35 40 45

Glu Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala
 50 55 60

Gln Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn
 65 70 75

Ile Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val
 80 85 90

Tyr Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu
 95 100 105

Asp Ala Leu Asp Leu Trp
110 115

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6

seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Ser Pro Phe Leu Ala Arg
 -110 -105 -100

Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
 -95 -90 -85

Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
 -90 -75 -70

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
 -65 -60 -55 -50

Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
 -45 -40 -35

Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys
 -30 -25 -20

Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser
 -15 -10 -5

Gly Leu Ile His Arg Val Cys Val Thr Thr Cys Phe Ile Phe Ser Met
 1 5 10 15

Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser
 20 25

(xii) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LMSLLLVLPVVEA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 -20 -15 -10

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

-5

1

5

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Val Pro Ala Trp
10 15 20

Gly Tyr Met His Gly
25

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq ILVVLMLPLAQA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
-20 -15 -10 -5

Leu Ala Gln Ala Leu Asp Cys His Val Cys Xaa Tyr Asn Gly Asp Asn
1 5 10

Cys

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11

seq LLALSLLVLWTSP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
-15                -10                -5

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
 1              5              10              15

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
              20              25              30

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
      35              40              45

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
      50              55              60

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Xaa Arg
      65              70              75              80

Ser Ser Xaa Pro Met Xaa Val Xaa Arg Glu Pro Glu Ser Glu Ser Ser
              85              90              95

Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa Arg
      100              105

```

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq RLLLLPLLLAVSG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
-20                -15                -10

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
-5              1              5              10

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met

```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10
seq LCRALCLFPRVFA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```
Met Glu Val Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu  
-20 -15 -10
```

```
Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser  
-5 1 5
```

```
Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro  
10 15 20
```

```
Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys  
25 30 35 40
```

```
Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Ile Ser Val Arg Arg  
45 50 55
```

```
Gln Leu
```

2: INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: AMINO ACID
 (C) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -19..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.5
 seq LMCLSLCTAFALS/KP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 1 5 10

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Xaa Tyr Asp
 15 20 25

His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa Phe Asp Gln Leu
 30 35 40 45

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 50 55 60

Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: AMINO ACID
 (C) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Substantia nigra
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -30..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.5
 seq LLFLSQFCILSGG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
 -30 -25 -20 -15

Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
 -10 -5 1

Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 5 10 15

Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser Thr Thr Asn Phe Ser Cys
 20 25 30

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Xaa Val Lys Pro Ser Val
 35 40 45 50

Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Xaa Phe Ile Ile Asn
 55 60 65

Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile

45

50

55

Xaa Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
60 65 70 75

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
80 85 90

Gly Leu Ser Gly Lys Trp
95

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq LLWLALACSPVHT/XL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val His Thr Xaa Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.3
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
  -15                -10                -5

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
   1                5                10                15

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ile Met Met Xaa Leu Gly Xaa
      20                25                30

Xaa Phe Thr Ile Asp Tyr Xaa Ile Phe Glu Ser Glu
      35                40

```

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.3
seq VLPVILLLLGAMP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
  -20                -15                -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
   -5                1                5                10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
      15                20                25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
      30                35                40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
      45                50                55

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
      60                65                70                75

```

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu
80 85

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: brain
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.2
seq LLXLALACSPVHT/TL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Arg Thr Leu Phe Asn Leu Leu Xaa Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
1 5 10

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
15 20 25

Gly Leu Val Val Thr Asp Gly
30 35

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -40..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9

seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```

Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
-40          -35          -30          -25

Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
          -20          -15          -10

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa
          -5          1          5

Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro
          10          15          20

Cys Thr Gly Gly Met Glu
          25          30

```

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

```

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
          -25          -20          -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
          -10          -5          1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
          5          10          15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
          20          25          30          35

Val Lys Pro His Met
          40

```


(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq SAVLSGFVLGALA/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu Gly
      -15                      -10                      -5

Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu Gly Phe
      1                      5                      10

Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile Thr Asp Ser
      15                      20                      25

Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp Ile Gln Lys Tyr
      30                      35                      40                      45

Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn Ser Ser Gly Glu Val
      50                      55                      60

Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser Asn Val Lys Lys Asn Val
      65                      70                      75

Val Gly Trp Tyr Lys Phe Arg Arg His Ser Asp Gln Ile Met Thr Phe
      80                      85                      90

Arg Glu Arg Leu Leu His Lys Asn Leu Gln Glu His Phe Ser Asn Gln
      95                      100                     105

Asp Leu Val Phe Leu Leu Leu Thr Pro
110                      115

```

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -32..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.8
 seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
   -30                      -25                      -20

Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
   -15                      -10                      -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
    1                      5                      10                      15

Asp Pro Glu Arg
          20
```

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -136..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.7
 seq AVALSLFLGWLGA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```
Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser Ala Pro Glu Ala Val Thr
   -135                      -130                      -125

Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
   -120                      -115                      -110                      -105

Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
   -100                      -95                      -90
```

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 -85 -80 -75
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 -70 -65 -60
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn
 -55 -50 -45
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
 -40 -35 -30 -25
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser
 -20 -15 -10
 Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg Phe
 -5 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq LLWLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Thr Ser Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq ASLFLLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
-40 -35 -30
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
-25 -20 -15
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
-10 -5 1 5
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
10 15 20
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
25 30 35
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser
40 45

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
seq LVLGLVLPILWA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Val Ala Pro Gly Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu
-15 -10 -5
Trp Ala Asp Arg Ser Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile
1 5 10

```

Asn Asn Asp Met Val Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp
 15                      20                      25                      30
Gly Phe Gly Thr Pro Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly
                      35                      40                      45
Gln Glu Thr Ile Met Lys Lys Val Thr Ser Val Lys Ala His Ser Asp
                      50                      55                      60
Thr Trp Met Val Val Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu
                      65                      70                      75
Val Met Ala Gln Gln Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val
                      80                      85                      90
His Asp Val Leu Phe Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn
                      95                      100                      105                      110
Met Gln Met Thr Ala Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu
                      115                      120                      125
Leu

```

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq LLTIVGLILPTRG/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
-20                      -15                      -10
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
-5                      1                      5                      10
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
15                      20                      25
Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
30                      35                      40

```

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
 45 50 55
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr Pro Arg
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LALSSLLSLLLFA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe Leu Ala Arg
 -45 -40 -35
 Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
 -30 -25 -20
 Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
 -15 -10 -5 1
 Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
 5 10 15
 Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
 20 25 30
 Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys
 35 40 45
 Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser
 50 55 60 65
 Gly Pro

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.3
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln
-35 -30 -25 -20

Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg
-15 -10 -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
1 5 10

Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly
15 20 25

Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe
30 35 40 45

Ile Glu Cys Glu Asp Arg
50

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -53..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.1
seq IYALFLLVGVCVA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

```

Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys
      -50              -45              -40

Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly
      -35              -30              -25

Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val
      -20              -15              -10

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln
      -5              1              5              10

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro
      15              20              25

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly
      30              35              40

Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys
      45              50              55

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe
      60              65              70

```

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -57..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq IVRLVAFCPFASS/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

```

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu
      -55              -50              -45

Leu Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val
      -40              -35              -30

Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu
      -25              -20              -15              -10

Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala
      -5              1              5

```


Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu
 10 15 20
 Glu Thr His Leu Pro Ser Lys Lys Lys Val Leu Leu Gly Val Gly
 25 30 35
 Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys
 40 45 50 55
 Gln Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Xaa Val Arg Leu His
 60 65 70
 Phe His Asn Leu Val Lys Gly Ser Asp Arg Cys Xaa Gln Leu Val Lys
 75 80 85
 His Ser Trp Gly Trp Asp Thr Ala Ile Pro Met
 90 95

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser
 -45 -40 -35
 Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser
 -30 -25 -20
 Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
 -15 -10 -5 1
 Pro Pro Tar Gln Pro Ser Pro Ala Ser Asp Ser Gly Ile Gly
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
-25 -20 -15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
-10 -5 1 5

Gln Glu Pro Leu His Asn Glu Glu Pro Gly
10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -48..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

-15

-10

-5

Leu Pro Thr Gln Xaa Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 1 5 10 15
 Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 20 25 30
 Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 35 40 45
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 50 55 60
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 65 70 75 80
 Pro Pro Leu

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa Xaa Ala
 -65 -60 -55
 Val Thr Ala Xaa Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
 -50 -45 -40
 Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
 -35 -30 -25
 Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro
 -20 -15 -10
 Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys
 -5 1 5 10
 Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
 15 20 25

Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Ala
 30 35 40
 Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg
 45 50 55
 Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe
 60 65 70 75
 Leu Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq LLMLLLFLSELQY/YL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr
 -45 -40 -35
 Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile
 -30 -25 -20
 Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr
 -15 -10 -5
 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg
 1 5 10 15
 Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro
 20 25 30
 Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln
 35 40 45
 Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly
 50 55 60
 Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu
 65 70 75 80

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro
85 90

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
-15 -10 -5

Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe Asp Trp Arg
1 5 10 15

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
20 25 30

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
35 40 45

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
50 55 60

Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
65 70 75 80

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe Asn Asp Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
 -15 -10 -5
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
 1 5 10
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met
 15 20 25
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu
 30 35 40 45
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala
 50 55 60
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
 65 70 75
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile
 80 85 90
Ala Cys Lys Leu Cys
 95

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
      -15                      -10                      -5
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
      1                      5                      10
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met
      15                      20                      25
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu
      30                      35                      40                      45
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Xaa
      50                      55                      60
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
      65                      70                      75
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile
      80                      85                      90
Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile
      95                      100                      105
Glu Ala Glu
110

```

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4
seq ILPLLFGCLGVFG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
      -20                      -15                      -10

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5              1              5              10
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15              20              25
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30              35              40
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45              50              55
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60              65              70              75
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80              85              90
Glu Ile Cys Ser
95

```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LLLVTWVFTPVT/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu
-25              -20              -15
Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
-10              -5              1
Ser Leu Asp Thr Glu Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
5              10              15

```

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr
-20 -15 -10 -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp
1 5 10

Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe
15 20 25

Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Phe Arg
30 35 40

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq ALSLLLVSGLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
-15 -10

Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro

-5

1

5

```

Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu
 10                      15                      20                      25
Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr
                      30                      35                      40
Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys
                      45                      50                      55
Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp
                      60                      65                      70
Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala
                      75                      80                      85
Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys
                      90                      95                      100                      105
Arg Ser Xaa Asn Lys Asn Glu Gly Gln Asp
                      110                      115

```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36...-1
- (D) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq IMLLSLAAFSVIS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly
-35                      -30                      -25
Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe
-20                      -15                      -10                      -5
Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val
                      1                      5                      10
Thr Ile Ser Ile Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys
                      15                      20                      25
Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr

```

30

35

40

Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His
 45 50 55 60

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Xaa Gly Ser Val Glu Cys Thr Xaa Gly Trp Gly His Cys Ala Pro
 -30 -25 -20

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
 20 25 30

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45

Val Met Val Ala Thr Asn Thr Pro Pro Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -25 -20 -15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 -10 -5 1
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 5 10 15
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 20 25 30 35
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa Gly Ala Lys Xaa
 40 45 50
Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 55 60 65
Phe

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Arg Tyr Ser Val Glu Cys Thr Trp Gly Xaa Gly His Cys Ala Pro
 -25 -20
Ser Pro Ile Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

-15

-10

-5

Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Xaa Val Gly Thr
 20 25 30
 Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45
 Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp
 50 55 60
 Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro
 65 70 75 80
 Lys Asp Ser Ile Gln Phe Ser Ser
 85

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq LRLKLAATSASA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ala Leu Arg Leu Leu Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg
 -15 -10 -5 1
 Val Val Ala Ala Gly Ala Gln Arg Val Arg Gly Ile His Ser Ser Val
 5 10 15
 Gln Cys Lys Leu Arg Tyr Gly Met Trp His Phe Leu Leu Gly Asp Lys
 20 25 30
 Ala Ser Lys Arg Leu Thr Glu Arg Ser Arg Val Ile Thr Val Asp Gly
 35 40 45
 Asn Met
 50

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65 -60 -55 -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
-45 -40 -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
-30 -25 -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
-15 -10 -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
1 5 10 15

Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
20 25 30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
35 40 45

Val Trp Lys Thr
50

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -154..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

```

Met Ala Leu Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
      -150                      -145                      -140

Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Xaa Asp Gly Tyr
      -135                      -130                      -125

Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
      -120                      -115                      -110

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
      -105                      -100                      -95

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
      -90                      -85                      -80                      -75

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
      -70                      -65                      -60

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
      -55                      -50                      -45

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
      -40                      -35                      -30

Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
      -25                      -20                      -15

Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
      -10                      -5                      1                      5

Lys Ala Thr

```

(2) INFORMATION FOR SEQ ID NO: 417:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(12) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(13) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -70..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LAFSLPALPLAEL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

```

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
-70                               -65                               -60                               -55

Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
                               -50                               -45                               -40

Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
                               -35                               -30                               -25

Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
                               -20                               -15                               -10

Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
                               -5                               1                               5                               10

Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
                               15                               20                               25

Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
                               30                               35                               40

Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser
                               45                               50                               55
  
```

(x) INFORMATION FOR SEQ ID NO: 418:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(12) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(13) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.6
 seq KMVHLLVLSGAWG/MQ

(14) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

```

Met Ala Gln Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
                               -20                               -15                               -10

Leu Ala Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
  
```


	-5							1							5
Ser	Gly	Phe	Leu	Leu	Phe	Arg	Ser	Leu	Pro	Arg	His	Thr	Phe	Gly	Leu
	10					15					20				
Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile	Ser	Met	Gly	Cys
25					30					35					40
Ala	Phe	Ile	Asn	Xaa	Cys	Ile	Leu	Ala	Ser	Gln	His	Ala	Trp	Ala	Gln
				45					50					55	
Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr	Leu	Leu	Phe	Leu		
			60					65					70		

(2) INFORMATION FOR SEQ ID NO: 419:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -81..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
 seq LLLASGTTLFCTS/FY
```

## (01) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

```
Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly
 -80 -75 -70

Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Xaa Phe
-65 -60 -55 -50

Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His
 -45 -40 -35

Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro
 -30 -25 -20

Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr
 -15 -10 -5

Ser Phe Tyr Tyr Gln Ala Gln
 1 5
```

2 INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 46 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Testis
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.5  
 seq LLTLLPPPPPLYT/RH
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```

Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
-20 -15 -10

Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
-5 1 5 10

Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
15 20 25

```

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -20..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.5  
 seq ILFLLPSICSSNS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

```

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys
-15 -10 -5

Met Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val

```

1

5

10

Val Thr Thr Thr Xaa Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu  
 15 20 25

Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Xaa Lys Gly Thr  
 30 35 40

Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Xaa Phe  
 45 50 55 60

## (2) INFORMATION FOR SEQ ID NO: 422:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3  
seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr  
 -15 -10 -5

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu  
 1 5 10

Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr  
 15 20 25

Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg  
 30 35 40 45

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu  
 50 55 60

Gln Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu  
 65 70 75

Lys Gln Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu  
 80 85 90

Val Val Trp Val Asp  
 95

## (C) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq SSCVLLTALVALA/AY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala Leu Ala Ala  
-15 -10 -5 1  
Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp Pro Trp Lys  
5 10 15  
Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Gln Gln Val Ser Asn  
20 25 30  
Leu Ile His Tyr Leu Gly Leu Ser His His Leu Leu Ala Leu Asn Phe  
35 40 45  
Ile Ile Val Ser Phe Gly Lys Lys Ser Ala Trp Ser Ser Ala Gln Val  
50 55 60 65  
Lys Val Thr Asp Thr Asp Phe Asp Gly Val Glu Val Arg Val Phe Glu  
70 75 80  
Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys Arg Ser Val Val Tyr Ile  
85 90 95  
His Gly Xaa Gly Trp  
100

## (C) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: brain

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq GVGLVTLLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly  
-25 -20 -15  
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg  
-10 -5 1 5  
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu  
10 15 20  
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe  
25 30 35  
Arg Phe Ala Leu Pro Thr Ala His His Met  
40 45

## (2) INFORMATION FOR SEQ ID NO: 425:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: brain

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -69...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq ILLIVLFLDAVRE/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Thr Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile  
-65 -60 -55  
Gly Leu Ile Leu Ile Phe Cys Leu Pro Phe Ile Pro Pro Gln Arg Trp  
-50 -45 -40  
Thr Lys Ile Phe Ser Phe Asn Val Trp Gly Lys Ile Ala Thr Phe Trp

-35                      -30                      -25  
 Asn Lys Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu  
   -20                      -15                      -10  
 Asp Ala Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu  
   -5                      1                      5                      10  
 Lys Ser Ser Thr Ser Arg Pro Arg  
                          15

## (2) INFORMATION FOR SEQ ID NO: 426:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq FLDFCVYIPLSWG/FC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426: \*

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser  
 -85                      -30                      -75                      -70  
 Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg  
                          -65                      -60                      -55  
 Glu Val Ser Gly Gly Pro Gly Gly Arg Arg Pro Phe Arg Pro Leu Ala  
                          -50                      -45                      -40  
 Thr Glu Thr Phe Ser Leu Ala Val Gly Thr Phe Cys Ser Arg Glu Pro  
                          -35                      -30                      -25  
 Val Gln Ser Asn Asn Leu His Leu Phe Leu Asp Phe Cys Val Tyr Ile  
                          -20                      -15                      -10  
 Pro Leu Ser Trp Gly Phe Cys Pro Leu Gln Pro Ile Leu Ala  
                          -5                      1                      5

## (2) INFORMATION FOR SEQ ID NO: 427:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq AILGSTWVALTTG/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

```

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
 -20 -15 -10

Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
 -5 1 5

Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
 10 15 20

Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe
 25 30 35 40

His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu
 45 50 55

Ala Arg Ala Asp Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa
 60 65 70

Pro Phe Leu Cys Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro
 75 80 85

Gly

```

(3) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.2  
seq FLVSNMLLAAYG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

```

Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
 -20 -15 -10

Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
 -5 1 5 10

Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
 15 20 25

Trp Leu Asp Ala Gln Ser Gly
 30

```

(i) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq SVLVLLLLLAVLYE/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe His
 -40 -35 -30

Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu Val
 -25 -20 -15 -10

Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys Ala
 -5 1 5

Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser Gln
 10 15 20

Leu Tyr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser Phe
 25 30 35

Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly Gln
 40 45 50 55

```



Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met Leu  
60 65 70

Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val  
75 80 85

## (2) INFORMATION FOR SEQ ID NO: 430:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq VVXXSVLXTTCXS/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala  
-75 -70 -65 -60

Gln Ala Gln Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg  
-55 -50 -45

Leu Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile  
-40 -35 -30

Asp Ala Gly Xaa Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val  
-25 -20 -15

Xaa Xaa Ser Val Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu  
-10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LLAALMLVAMLQL/LY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```

Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr Gln Leu Leu Leu
 -25 -20 -15

Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu Tyr Leu Ser Leu
 -10 -5 1 5

Leu Ser Gly Leu His Gly Pro
 10

```

## (2) INFORMATION FOR SEQ ID NO: 432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq IILLIHTMQVCTT/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```

Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val
 -15 -10 -5

Cys Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro
 1 5 10

Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr Ala Pro Met
 15 20 25

Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro Glu
 30 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 433:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe  
-20 -15 -10  
Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile  
-5 1 5 10  
Leu Gln Cys Ser Val Gly Ile  
15

(2) INFORMATION FOR SEQ ID NO: 434:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -52..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq LMAFLLSFYLIFT/NE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys  
-50 -45 -40  
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr  
-35 -30 -25

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr  
-20 -15 -10 -5  
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu  
1 5 10  
Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val  
15 20 25  
Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile  
30 35 40

## (2) INFORMATION FOR SEQ ID NO: 435:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LEMLTAFASHIRA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr Ala Phe Ala  
-20 -15 -10  
Ser His Ile Arg Ala Arg Asp Ala Ser Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Val His Lys Pro Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile  
                  -20                  -15                  -10  
His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr  
                  -5                                  1                                  5  
Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro  
          10                                  15                                  20  
Thr Thr  
          25

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq IGLMFLMLGALP/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile  
                  -25                  -20                  -15  
Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys  
          -10                                  -5                                  1  
Tyr Trp Pro Thr  
          5

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6  
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

```
Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val
-20 -15 -10

Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr
-5 1 5 10

Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile
15 20 25

Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu
30 35 40

Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln
45 50 55

Met Arg Asn Ser Gln Ala His Arg
60 65
```

(2) INFORMATION FOR SEQ ID NO: 439:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -87..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9  
seq SNILLASVGSVLG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

```
Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
```

-85                      -80                      -75  
 Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly  
     -70                      -65                      -60  
 Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile  
     -55                      -50                      -45                      -40  
 Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln  
                     -35                      -30                      -25  
 Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala  
             -20                      -15                      -10  
 Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Xaa  
     -5                      1                      5  
 Ser Leu Pro Ala Glu Pro Xaa Xaa Xaa Glu Asp Glu Ala Arg Glu Asn  
     10                      15                      20                      25  
 Val Pro Pro

## (2) INFORMATION FOR SEQ ID NO: 440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq VTIIILLSCXFWA/VK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Val Thr Ile Ile Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys  
             -10                      -5                      1  
 Asn Val Thr Xaa Arg Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile  
     5                      10                      15

## (2) INFORMATION FOR SEQ ID NO: 441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lung

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -87..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.8  
seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Xaa Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val  
-85 -80 -75  
Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly  
-70 -65 -60  
Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile  
-55 -50 -45 -40  
Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln  
-35 -30 -25  
Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala  
-20 -15 -10  
Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser  
-5 1 5  
Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn  
10 15 20 25  
Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His  
30 35 40  
Glu Arg

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -89..-1



(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq DLSLLSLPPGTSP/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
 -85 -80 -75

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Xaa Xaa Gly Arg Asn
 -70 -65 -60

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu
 -55 -50 -45

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
 -40 -35 -30

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu
 -25 -20 -15 -10

Leu Ser Leu Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu
 -5 1 5

Ala Pro Ile Pro Pro Thr Xaa Leu Ala Xaa Ala Xaa Cys Trp Ala Pro
 10 15 20

Ser Val Arg Trp Thr Cys
 25

```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq LLLPRVLLTMASG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

```

Met Pro Xaa Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
 -20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Leu Arg Xaa Ser Xaa Arg Arg
 -5 1 5

```

Pro Arg Ile Pro Xaa Leu Ala Thr Phe Arg Xaa Arg Ser Leu  
 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq IFSFLDIVTLCRC/AQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro  
 -35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu  
 -15 -10 -5

Cys Arg Cys Ala Gln Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp  
 1 5 10

Gly Ser Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val  
 15 20 25

Glu Gly Arg Val Val Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu  
 30 35 40 45

Arg Lys Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu  
 50 55 60

Xaa Thr Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn  
 65 70 75

Gly Cys Thr Lys Ile Thr Xaa Ser Thr Cys  
 80 85

## (2) INFORMATION FOR SEQ ID NO: 445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7  
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro  
-35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu  
-15 -10 -5

Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp  
1 5 10

Gly Ser Asn Trp Gln Gly  
15

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -112..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6  
seq SSCILP#LSKTNS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu Pro Ser Asp Pro Gln  
-110 -105 -100

Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala Arg Ser Leu Pro  
-95 -90 -85

```

Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val Asp Trp Asp His
-30 -75 -70 -65

His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu Asn Leu Pro Arg
 -60 -55 -50

Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys Pro Val Cys Leu
 -45 -40 -35

Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met Pro Cys His His
 -30 -25 -20

Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser Lys Thr Asn Ser
-15 -10 -5

Cys Pro Leu Cys Arg Tyr Glu Leu Pro Thr Asp Asp Asp Thr Tyr Glu
 1 5 10 15

Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln Gln His Arg Pro
 20 25 30

Xaa

```

## (2) INFORMATION FOR SEQ ID NO: 447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LILSLQVCRPATL/DQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15 -10 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
 5 10 15

Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln Pro Ser Pro
 20 25 30

Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu Gln Pro Arg
 35 40 45

Pro Gly

```

50

## (2) INFORMATION FOR SEQ ID NO: 448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LRRLGCLTLTL/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Leu Gly Ile Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu  
-70 -65 -60

Gly Leu Glu Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly  
-55 -50 -45

Ser Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn  
-40 -35 -30

Glu Ala Arg Gly Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu  
-25 -20 -15 -10

Leu Gly Cys Leu Thr Leu Thr Leu Ser Gly Arg Ile  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6  
seq ALKLASWTSMALA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
 -15 -10 -5
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
 1 5 10 15
Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
 20 25 30
Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
 35 40 45
Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
 50 55 60
Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
 65 70

```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq AALPAWLSLQSR/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

```

Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser Arg Ala
 -15 -10 -5
Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr Pro Val
 1 5 10
Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro
 20 25 30
Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Arg Gln
 35 40 45

```

```

Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro Ser Ala
 50 55 60

Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro
 65 70 75 80

Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn Phe Leu
 85 90 95

His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu Lys Asp
 100 105 110

Phe Cys Thr Glu
 115

```

## (2) INFORMATION FOR SEQ ID NO: 451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CMLTLXXLSFILA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

```

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65 -60 -55 -50

Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
 -45 -40 -35

Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
 -30 -25 -20

Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
 -15 -10 -5

Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
 1 5 10 15

Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
 20 25 30

Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
 35 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LLLSFVWMPALLP/DG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser  
-45 -40 -35  
Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val Ala Ala Thr  
-30 -25 -20  
Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro  
-15 -10 -5  
Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LKGFLFXVIVLTS/NI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:



Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val Ile Val Leu  
                   -15                  -10                  -5

Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg Trp Gly Cys  
                   1                                  5                                  10

Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr Pro Asp Asn  
           15                                  20                                  25                                  30

Phe Cys Thr Tyr

## (2) INFORMATION FOR SEQ ID NO: 454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq VVEMTVAASGASS/FA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu  
                   -25                  -20                  -15

Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe Ala Val  
                   -10                                  -5                                  1

Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro  
           5                                  10                                  15

Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr  
           20                                  25                                  30                                  35

Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg  
                   40                                  45                                  50

Val Thr

## (2) INFORMATION FOR SEQ ID NO: 455:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5  
seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Glu Leu Ala His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln  
-15                      -10                      -5                      1  
Ile Thr Glu Ala Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe  
                    5                      10                      15  
Leu Asp Lys Val Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys  
                    20                      25                      30  
Gln Lys Lys Leu Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro  
                    35                      40                      45  
Gly Pro Thr Gly  
                    50

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5  
seq LGYLVLSEGAFLA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu  
                    -25                      -20                      -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp  
 -10 -5 1

Leu Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser  
 5 10 15 20

Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys  
 25 30 35

Arg Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser  
 40 45 50

Gly Gln Arg Val Phe Val Val Lys Arg Gly  
 55 60

## (2) INFORMATION FOR SEQ ID NO: 457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LVGVLFVSVTTG/PW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr  
 -30 -25 -20

Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro  
 -15 -10 -5 1

Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys  
 5 10 15

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn  
 20 25 30

Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val  
 35 40 45

Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa Ser Gly Asn  
 50 55 60 65

Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Ala Ile Ser  
 70 75 80

Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa Xaa Val Ser  
85 90 95  
Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys  
100 105 110  
Phe Gly Phe Val  
115

## (2) INFORMATION FOR SEQ ID NO: 458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq MVLLTMIARVADG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu  
-10 -5 1  
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg  
5 10 15

## (2) INFORMATION FOR SEQ ID NO: 459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq MVLLTMIARVADG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

```

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
 -10 -5 1
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg Asp Leu Gln Gln
 5 10 15
Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser
 20 25 30 35
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile
 40 45 50
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro
 55 60 65
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
 70 75 80
Glu Gln
 85

```

## (2) INFORMATION FOR SEQ ID NO: 460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq MMVLSLGIXLASA/SF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

```

Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55
Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40
Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
 -35 -30 -25
Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10

```

Xaa Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser  
 -5 1 5 10  
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile  
 15 20 25  
 Ile Ser Gly Ser Leu Ser Ile  
 30

## (2) INFORMATION FOR SEQ ID NO: 461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq AVTSLLSPTPATA/LA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser  
 -25 -20 -15 -10  
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser  
 -5 1 5  
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly  
 10 15 20  
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly  
 25 30 35  
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His  
 40 45 50 55  
 Val Gly Val Gly Lys Xaa Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile  
 60 65 70  
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu  
 75 80 85 90 95  
 Ala Val Xaa Leu Ile Thr Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys  
 90 95 100  
 Thr Phe Val Thr Trp Phe Leu  
 105 110

## (2) INFORMATION FOR SEQ ID NO: 462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq AVTSLLSPTPATA/LA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
-25 -20 -15 -10

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35

Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55

Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70

Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85

Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
 90 95 100

Thr Phe Val His Val Val Pro
 105 110

```

## (2) INFORMATION FOR SEQ ID NO: 463:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -57..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq AIALATVLFLLGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```
Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
 -55 -50 -45

Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
 -40 -35 -30

Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 -25 -20 -15 -10

Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
 -5 1 5

Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
 10 15 20

Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
 25 30 35
```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```
Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
```



```

-15 -10 -5 1
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
 5 10 15
Gln His Pro Thr Xaa Gln
 20

```

(2) INFORMATION FOR SEO ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 465:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp  
-15 -10 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln  
5 10 15

Gln His Pro Thr Gln Cys Ser Thr His Leu Gly  
20 25

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(13) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -68..-1  
(C) IDENTIFICATION METHOD: Von Holst matrix

(D) OTHER INFORMATION: score 5.2  
seq GVLLLLSSIHFC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

```

Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
 -65 -60 -55
Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
 -50 -45 -40
Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
 -35 -30 -25
Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
 -20 -15 -10 -5
His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
 1 5 10
Ala

```

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -94..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq VILQLQFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```

Met Phe Gly Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln
 -90 -85 -80
Arg Asp Ser Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly
 -75 -70 -65
Asp Val Val Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr
 -60 -55 -50
Leu Gln Gln Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly
 -45 -40 -35
Pro Gly Gln Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser

```

-30                      -25                      -20                      -15  
 Pro Val Ile Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr  
                          -10                      -5                      1  
 Leu Ser Leu Lys Leu Val His Val Ala Gly Pro Gly Pro Thr  
                          5                      10                      15

## (2) INFORMATION FOR SEQ ID NO: 468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq LILVGTSKHVAFG/KI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu  
   -85                      -80                      -75  
 Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly  
  -70                      -65                      -60                      -55  
 Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp  
                          -50                      -45                      -40  
 Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu  
                          -35                      -30                      -25  
 Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser  
                          -20                      -15                      -10  
 Lys His Val Ala Phe Gly Lys Ile Ile  
                          -5                      1

## (2) INFORMATION FOR SEQ ID NO: 469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -35..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq WYSTVGLLPPVRA/MS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys Asp His Gly Thr
-35 -30 -25 -20

Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly Leu Leu Pro Pro
 -15 -10 -5

Val Arg Ala Met Ser Gln Arg Asn Leu Asn
 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -36..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq ARALAALVPGVTQ/VD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Ala Ala Ala Leu Lys Cys Leu Leu Thr Leu Gly Arg Trp Cys Pro
-35 -30 -25

Gly Leu Gly Val Ala Pro Gln Ala Arg Ala Leu Ala Ala Leu Val Pro
-20 -15 -10 -5

Gly Val Thr Gln Val Asp Asn Lys Ser Gly Phe Leu Gln Lys Arg Pro
 1 5 10

His Arg Gln His Pro Gly Ile Leu Lys Leu Phe His Val Arg Leu Pro
 15 20 25

```

Gln Ala Leu Ala Asn Gly Ala Gln Leu Leu Leu Gly Ser Ala Gly  
 30 35 40

Pro Thr Met Glu Asn Gln Val Gln Thr Leu Thr Ser Tyr Leu Trp Ser  
 45 50 55 60

Arg His Leu Pro Val Glu Pro Xaa Glu Leu Gln Arg Arg Ala Xaa His  
 65 70 75

Leu Glu Lys Lys Phe Leu Glu Asn Pro Asp Leu Ser Gln Thr Glu Glu  
 80 85 90

Lys Leu Arg Gly Ala Gly  
 95

## (2) INFORMATION FOR SEQ ID NO: 471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -102..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq TVMSALSVAPSKA/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu Ile Lys Gly Ser  
 -100 -95 -90

Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly  
 -85 -80 -75

Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val  
 -70 -65 -60 -55

Pro Pro Ala Met Xaa Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly  
 -50 -45 -40

Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile  
 -35 -30 -25

Arg Asp Ser Trp Xaa Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser  
 -20 -15 -10

Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr  
 -5 1 5 10

Val Lys Ala Leu Gly  
15

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Val Asn Glu Leu Gln Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala  
-15 -10 -5

Cys Ser Ser Ser Lys Gln Arg Phe  
1 5

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq FFFSIQPFLLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala Phe Phe Phe Ser Ile

-10

Leu Xaa Thr Ser Pro Trp  
25 30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 99 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -70..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.9  
 seq LVFVLLFIFVKRQ/IM
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

```

Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
-70 -65 -60 -55

Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
 -50 -45 -40

Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn
 -35 -30 -25

Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe
 -20 -15 -10

Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg
 -5 1 5 10

Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn
 15 20 25

Tyr Leu Tyr

```

(2) INFORMATION FOR SEQ ID NO: 476:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -56..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.9



seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
-55 -50 -45

Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser
-40 -35 -30 -25

Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
 -20 -15 -10

Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly
 -5 1 5

Pro Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro
10 15 20

Phe Val
25

```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Glu Glu Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys
-25 -20 -15

Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
-10 -5 1 5

Ser Val Arg Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser
10 15 20

Lys His Leu Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp
25 30 35

```

Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys  
 40 45 50

## (2) INFORMATION FOR SEQ ID NO: 478:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LXXVVAFVAPGES/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Val Arg Arg Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu  
 -15 -10 -5

Ser Gln Gln Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly  
 1 5 10 15

Gln Glu Arg Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly  
 20 25 30

Asp Cys Gln Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp  
 35 40 45

Gly Ser Asp Val Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys  
 50 55 60

Thr Lys Glu Ala Gly Asp Gly Pro Leu  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 479:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq PIVRLLSCP GTVA/KD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn Leu Cys Ala  
-35 -30 -25

Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu Leu Ser Cys  
-20 -15 -10

Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln Pro Ser Gly  
-5 1 5 10

Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg Arg Phe Ser  
15 20 25

Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr Val Leu Ile  
30 35 40

His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys Tyr Leu Ser  
45 50 55

Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser Phe Gly Leu  
60 65 70 75

Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly Ser Leu Gln  
80 85 90

Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala Ile Pro Phe  
95 100 105

Arg Ser Arg Ser Ser  
110

## (2) INFORMATION FOR SEQ ID NO: 480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LVILSLKSQT LDA/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
-60 -55 -50 -45

Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
 -40 -35 -30

Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
 -25 -20 -15

Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
 -10 -5 1

Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
 5 10 15 20

Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Xaa
 25 30 35

Asn Met Asn Leu Glu Gly Gly
 40

```

## (2) INFORMATION FOR SEQ ID NO: 481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLVHLLCQNQVLG/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly Asp Ser Gly
 -30 -25 -20

Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn Gln Val Leu
 -15 -10 -5

Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His
 1 5 10 15

Asp Tyr Lys Glu Gly Thr Pro Gln Glu Lys Thr Tyr Tyr Ile Glu Leu
 20 25 30

```

Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr  
                   35                  40                  45  
 Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa Val His Asp  
                   50                  55                  60  
 Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp Ser Leu Glu  
                   65                  70                  75  
 Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val  
                   80                  85                  90

## (2) INFORMATION FOR SEQ ID NO: 482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq WAFSCGTWLPRA/EW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly  
       -30                  -25                  -20  
 Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu  
       -15                  -10                  -5                  1  
 Trp Leu Leu Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile  
                   5                  10                  15  
 Gly Gln Phe Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg  
                   20                  25                  30  
 Leu Met Ile Arg Lys Leu Val Ala Glu Asn Arg  
       35                  40

## (2) INFORMATION FOR SEQ ID NO: 483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Surrénals

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met  
-25 -20 -15  
Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe  
-10 -5 1 5  
Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro  
10 15 20  
Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu  
25 30 35  
Cys Ala Arg  
40

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -31..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys  
-30 -25 -20  
Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala

BNSDOCID: <WO\_9906548A2\_1\_>

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LSLXASYIFGISG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
 -70 -65 -60

Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
 -55 -50 -45

Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
 -40 -35 -30 -25

Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
 -20 -15 -10

Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
 -5 1 5

Arg Asn Glu Phe Val Arg Gln Ser
 10 15

```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -76..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
 -75 -70 -65

Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
 -60 -55 -50 -45

Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
 -40 -35 -30

Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Xaa Leu
 -25 -20 -15

```



Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser  
 -10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: S adrenals

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq SVMGVCLLIPGLA/TA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Trp Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu  
 -20 -15 -10  
 Leu Ile Pro Gly Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg  
 -5 1 5 10  
 Gly Lys Glu Lys Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met  
 15 20 25  
 Glu Arg Asp Arg Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys  
 30 35 40  
 Gl, Pro Gly  
 45

## (2) INFORMATION FOR SEQ ID NO: 489:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -46..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Glu Phe Lys Leu Glu Ala His Arg Ile Val Ser Ile Ser Leu Gly
-45 -40 -35

Lys Ile Tyr Asn Ser Arg Val Gln Arg Gly Gly Ile Lys Leu His Lys
-30 -25 -20 -15

Asn Leu Leu Val Ser Leu Val Leu Arg Xaa Pro Ala Lys Ser Thr Arg
-10 -5 1

Ala Gly

```

(xii) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -97..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq IASGLGLXLDGWT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
-95 -90 -85

Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
-80 -75 -70

Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
-65 -60 -55 -50

Gln Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
-45 -40 -35

Gln Val Tyr Pro Xaa Phe Leu Phe Phe Leu Ala Val Gly Gly Val
-30 -25 -20

Pro Arg Ile Ala Ser Gly Leu Gly Leu Xaa Leu Asp Cys Trp
-15 -10 -5

```

Thr Ser Ser Leu Cys Leu Trp Leu Leu His Gly Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq RIPS LPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala  
-40 -35 -30  
Met Ser Ser Trp Ala Arg Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro  
-25 -20 -15  
Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp  
-10 -5 1

.. INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq RLLRRFLASVIS/RK

.. SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser  
 -15 -10 -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu  
 1 5 10 15

Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro  
 20 25 30

Ala Arg Thr  
 35

## (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq FLLLEVSHELLLI/IN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe Leu Leu Leu  
 -25 -20 -15 -10

Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu Gly  
 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 494:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -77..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
 seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

```

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 -75 -70 -65

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
 -60 -55 -50

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
 -45 -40 -35 -30

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
 -25 -20 -15

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
 -10 -5 1

```

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
 seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
 -20 -15 -10

Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
 -5 1 5 10

Val Tyr Tyr Arg Gly Gly Val
 15

```

... INFORMATION FOR SEQ ID NO: 496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq LVFMVPLVGLIHL/GW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25 -20 -15 -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20

Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
 25 30 35
```

## (2) INFORMATION FOR SEQ ID NO: 497:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq VFCLLISIPTPSA/HL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
Met Gly Trp Asp Gly Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile
```

-20                      -15                      -10  
 Ser Ile Pro Thr Pro Ser Ala His Leu  
       -5                      1

## (2) INFORMATION FOR SEQ ID NO: 498:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -118..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq ILAHLRLGLIPIHA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala Trp Phe Trp  
       -115                      -110                      -105  
 Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe Pro Val Thr  
       -100                      -95                      -90  
 Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe Glu Xaa Arg  
       -85                      -80                      -75  
 Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser Leu Glu Phe  
       -70                      -65                      -60                      -55  
 Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe Arg Arg Ile  
       -50                      -45                      -40  
 Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val Leu Val Tyr  
       -35                      -30                      -25  
 Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His Arg Leu Gly  
       -20                      -15                      -10  
 Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr Arg Asn Gln  
       -5                      1                      5                      10  
 Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe Arg Leu Gln  
       15                      20                      25  
 Val Arg Cys Thr Arg  
       30

## (2) INFORMATION FOR SEQ ID NO: 499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -77..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq FEARIALLPLLQA/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
 -75 -70 -65

Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
 -60 -55 -50

Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
 -45 -40 -35 -30

Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
 -25 -20 -15

Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
 -10 -5 1

Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
 5 10 15

Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa Xaa Val Pro
 20 25 30 35

His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:



(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq VLFFTGWWIIIDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp  
-40 -35 -30  
Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe  
-25 -20 -15  
Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr  
-10 -5 1 5  
Arg

## (2) INFORMATION FOR SEQ ID NO: 501:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -44..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LVFLTFLSIPSFV/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Met Thr Gln Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg  
-40 -35 -30  
Ile Ile Cys Ser Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu  
-25 -20 -15  
Val Phe Leu Thr Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn  
-10 -5 1  
Ile Arg Ala Glu Thr Phe Leu Gln Asn Val  
5 10

## (2) INFORMATION FOR SEQ ID NO: 502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq FLTALLWRGRIPG/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln  
                  -10                  -5                  1

Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys  
          5                          10                  15

Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp  
  20                          25                  30

Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa  
  35                          40                  45                  50

Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser  
                  55                          60                  65

Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Xaa  
          70                          75                  80

Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu  
          85                          90                  95

Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys  
  100                          105                  110

Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr  
  115                          120                  125

## (2) INFORMATION FOR SEQ ID NO: 503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala  
-90 -85 -30 -75

Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly  
-70 -65 -60

Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln  
-55 -50 -45

Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr  
-40 -35 -30

Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu  
-25 -20 -15

Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LIVNLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

```

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu
 -50 -45 -40

Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val Leu Leu Pro
 -35 -30 -25

Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp Leu Leu Val
 -20 -15 -10

Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
 -5 1 5 10

Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
 15 20 25

Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
 30 35 40

Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys His Arg Xaa
 45 50 55

Leu His His Tyr Tyr Gly Cys
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq CPTCLCAPSXXWG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu Pro
 -10 -5 1

Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys Lys
 5 10 15

Ala Arg Ser
 20

```

## (2) INFORMATION FOR SEQ ID NO: 506:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 amino acids  
    (B) TYPE: AMINO ACID  
    (C) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Brain
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -19..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.2  
                            seq AVAASAASGQAEG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln  
                  -15                  -10                  -5  
Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser  
                  1                          5                          10  
Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu  
          15                          20                          25  
Ile Ser Arg Leu Arg  
          30

(2) INFORMATION FOR SEQ ID NO: 507:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -17..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.2  
                            seq SLLXRVSVTAVAA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Ala Ala Met Ser Leu Leu Xaa Arg Val Ser Val Thr Ala Val Ala

-15

-10

-5

Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa Leu Gly Phe Gly Gly Phe  
 1 5 10 15  
 Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala Pro Val Arg His Ser Gly  
 20 25 30  
 Asp His Gly Lys Arg Leu Phe Val Ile Arg Pro Ser Arg Phe Tyr Asp  
 35 40 45  
 Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr Ile Ala Leu Thr Gly Ile  
 50 55 60  
 Pro Val Ala Xaa Phe Ile Thr Leu Val Asn Val Phe Ile Gly Gln Ala  
 65 70 75  
 Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val Pro Glu His Trp Glu Tyr  
 80 85 90 95  
 Tyr Lys His Pro Ile Ser Arg Trp Ile Ala Arg Asn Phe Tyr Asp Ser  
 100 105 110  
 Pro Xaa Lys Ile Tyr Glu Arg Thr Met  
 115 120

## (2) INFORMATION FOR SEQ ID NO: 508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LDLLRGLPRVSLA/NL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu  
 -25 -20 -15 -10  
 Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly  
 -5 1 5  
 Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Gly Arg Lys  
 10 15 20  
 Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg

25                      30                      35  
 Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys  
 40                      45                      50                      55  
 Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu  
                     60                      65                      70  
 Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro  
                     75                      80                      85  
 Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr  
                     90                      95                      100  
 Ile Ala Pro  
 105

## (2) INFORMATION FOR SEQ ID NO: 509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq GILILWIIRLLFS/KT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala  
 -40                      -35                      -30  
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile  
 -25                      -20                      -15                      -10  
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu  
                     -5                      1                      5  
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp  
                     10                      15                      20  
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu  
                     25                      30                      35  
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn  
                     40                      45                      50                      55

Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu  
                                 60                                65                                70  
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr  
                                 75                                80                                85  
 Gly Val Gly Thr Cys Gly Pro Cys  
                                 90                                95

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq QGVLFICFTCARS/FP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Glu Asp Pro Asn Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro  
                                 -75                                -70                                -65  
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly  
                                 -60                                -55                                -50  
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa  
                                 -45                                -40                                -35  
 Xaa Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln  
                                 -30                                -25                                -20  
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe  
                                 -15                                -10                                -5                                1  
 Pro Ser

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN



(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -32..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

```
Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
 -30 -25 -20

Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
 -15 -10 -5

Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
 1 5 10 15

His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
 20 25 30

Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr Ser
 35 40 45

Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser Gln
 50 55 60

Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys Tyr
 65 70 75 80

Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly Xaa
 85 90 95

Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -58..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1  
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

```

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
 -55 -50 -45

Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr Gly
 -40 -35 -30

Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
 -25 -20 -15

His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
 -10 -5 1 5

Ala Tyr Leu Pro Thr Gly Lys Trp
 10

```

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

```

Met Ala Thr Leu Thr Phe Ser Leu Arg Lys Pro Leu Gln Arg Ser Leu
 -85 -80 -75

Ile Arg Pro Ser His Leu Pro Leu Cys Cys Phe Asp Trp Arg Leu Ser
 -70 -65 -60

His Tyr Tyr Arg Leu Pro Pro Ala Val Arg Leu His Gln Gln Arg Gly
 -55 -50 -45

Gly Arg Pro Gly Arg Ser Ser Ala Asp His Trp His Ser Gly Val Pro
 -40 -35 -30 -25

Thr Arg Ile Leu Pro Pro Ala His Arg Leu Leu Cys Ile Gln Arg Leu
 -20 -15 -10

```

Pro Trp Leu Leu Leu Cys Arg Gly Ile Thr Ser  
           -5                                  1

## (2) INFORMATION FOR SEQ ID NO: 514:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq PSLAAGLLFGSXA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Lys | Pro | Leu | Phe | Pro | Leu | Val | Pro | Leu | His | Trp | Phe | Gly | Phe |  |
|     |     |     |     | -45 |     |     |     | -40 |     |     |     |     |     | -35 |     |  |
| Gly | Tyr | Thr | Ala | Leu | Val | Val | Ser | Gly | Gly | Ile | Val | Gly | Tyr | Val | Lys |  |
|     |     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |  |
| Thr | Gly | Ser | Val | Pro | Ser | Leu | Ala | Ala | Gly | Leu | Leu | Phe | Gly | Ser | Xaa |  |
|     |     | -15 |     |     |     | -10 |     |     |     |     |     | -5  |     |     |     |  |
| Ala | Gly | Leu | Gly | Ala | Tyr | Gln | Leu | Tyr | Gln | Asp | Pro | Arg | Asn | Val | Trp |  |
|     | 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Gly | Phe | Leu | Ala | Ala | Thr | Ser | Val |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO: 515:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
 seq VAVGLTIAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

```

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly
 -15 -10 -5

Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln
 1 5 10

Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
 15 20 25 30

Tyr Tyr Arg Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala
 35 40 45

Gly

```

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -83..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
 seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

```

Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
 -30 -75 -70

Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
 -65 -60 -55

Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
 -50 -45 -40

Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Val Gln Gly Pro
 -35 -30 -25 -20

His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg Leu Leu Ser Gln
 -15 -10 -5

```

Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe Ser Gln Tyr Cys  
                  1                                  5                                  10  
Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe Phe Phe  
         15                                  20                                  25

## (2) INFORMATION FOR SEQ ID NO: 517:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq ITSSLFLGRGSA/SN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala Pro  
         -40                                  -35                                  -30  
Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr Ser  
         -25                                  -20                                  -15  
Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu Leu  
         -10                                  -5                                  1                                  5  
Gln Ala Arg Gly Ile  
                                  10

## (2) INFORMATION FOR SEQ ID NO: 518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly Thr  
-15 -10 -5  
Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe Leu  
1 5 10  
Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser Asp  
15 20 25 30  
Phe Glu Lys Val Gln Glu Arg  
35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq ILFHGVFYGGA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly  
-15 -10 -5  
Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr  
1 5 10  
Leu

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr  
-10 -5 1  
Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val  
5 10 15  
Glu Xaa Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe  
20 25 30 35  
Asp Asp Leu Pro Ala Arg Phe Gly Tyr  
40

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala  
-25 -20 -15 -10  
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys  
-5 1 5  
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His  
10 15 20

Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp  
 25 30 35  
 Xaa Xaa Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe  
 40 45 50 55  
 Pro Phe Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu  
 60 65 70

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq YTAVSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg  
 -60 -55 -50  
 Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn  
 -45 -40 -35 -30  
 Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu  
 -25 -20 -15  
 Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln  
 -10 -5 1  
 Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His  
 5 10 15  
 Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn Gly Arg  
 20 25 30 35  
 Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala  
 40 45

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```
Met Ala Ile Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser
-30 -25 -20 -15

Lys Leu Trp Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile
 -10 -5 1

Xaa Ala Glu Pro Pro Gln Leu Asp Ile Ser
 5 10
```

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq FVLGSARLGGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```
Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu Asp Asp Phe Val
 -25 -20 -15

Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met Arg Pro Ala Ala
-10 -5 1 5

Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu Pro Asn Gln Leu
```

10

15

20

Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg Val Arg Thr Ala  
25 30 35

Thr

## (2) INFORMATION FOR SEQ ID NO: 525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LVSATAWLEECWW/SE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Lys Leu Val Ser Ala Thr Ala Trp Leu Glu Glu Cys Trp Trp Ser  
-15 -10 -5 1

Glu Leu Ser

## (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LYVPLLA VCCLHS/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

BNSDOCID: &lt;WO\_\_9906548A2\_I\_&gt;

## (2) INFORMATION FOR SEQ ID NO: 528:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -100..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq LASSFLFTMGGLG/FI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn  
-100 -95 -90 -85

Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr  
-80 -75 -70

Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile  
-65 -60 -55

Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp  
-50 -45 -40

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn  
-35 -30 -25

Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met  
-20 -15 -10 -5

Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile  
1 5 10

Pro Lys Leu Asn Arg Phe  
15

## (2) INFORMATION FOR SEQ ID NO: 529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -13..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq MLVLRSGLTALA/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr  
-10 -5 1  
Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val Arg Lys Ala  
5 10 15  
Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile Pro Asn Leu  
20 25 30 35  
Ala Arg Ile Asp Lys Gln Glu Thr Arg  
40

## (2) INFORMATION FOR SEQ ID NO: 530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -36..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq NIESLAWTGGTLG/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Ala Ala Pro Leu Ser Val Glu Val Glu Phe Gly Gly Gly Ala Xaa  
-35 -30 -25  
Ser Cys Leu Thr Val Leu Arg Asn Ile Glu Ser Leu Ala Trp Thr Gly  
-20 -15 -10 -5  
Gly Thr Leu Gly His Pro Glu Pro Ala His Leu Asp Gln Glu Glu Phe  
1 5 10  
Ala Lys Arg Ala Ala Xaa Val Val His Pro Gly Arg Gln Arg Ala Ala

15

20

25

Arg Asn Ser Gly Ala Asp Tyr Arg  
 30 35

## (2) INFORMATION FOR SEQ ID NO: 531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq FVGGLPVIFWSNA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Thr His Leu Ile Glu Tyr Asp Arg His Arg Lys Ser Arg Leu Ser  
 -65 -60 -55 -50

Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp His Ser Arg Asn Ala  
 -45 -40 -35

Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro Pro Thr Val Asp Ser  
 -30 -25 -20

Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val Ile Phe Trp Ser Trp  
 -15 -10 -5

Ala Gly Leu Val  
 1

## (2) INFORMATION FOR SEQ ID NO: 532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Ala Ala Ala Ala Leu Gly Gln Ile Trp Ala Arg Lys Leu Leu Ser  
-20 -15 -10  
Val Pro Trp Leu Leu Cys Gly Pro Arg Arg Tyr Ala Ser Ser Ser Phe  
-5 1 5 10  
Lys Ala Ala Asp Leu Gln Leu Glu Met Thr Gln Lys Pro His Lys Lys  
15 20 25  
Pro Gly Pro Gly Glu Pro Leu Val Phe Gly Lys Thr Phe Thr Asp His  
30 35 40  
Met Leu Met Val Glu Trp Asn Asp Lys Gly Trp Gly Gln Pro Arg Ile  
45 50 55  
Gln Pro Phe Gln Asn Leu Thr Leu His Pro Ala Ser Ser Ser Leu His  
60 65 70  
Tyr Ser Leu Gln Leu Phe Glu Gly  
75 80

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq CPLLLLVTNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Ala Val Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro  
-35 -30 -25  
Glu Lys Pro Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Leu Val  
-20 -15 -10

```

Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg
-5 1 5 10
Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala
 15 20 25
Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala
 30 35 40
Arg Xaa Lys Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val
 45 50 55
Lys Arg Pro
 60

```

## (2) INFORMATION FOR SEQ ID NO: 534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq AVLDCAFYDPHTA/WS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

```

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
-20 -15 -10
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
-5 1 5 10
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25
Pro Leu Ser Asp Val Leu
 30

```

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -86..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala  
-85 -80 -75  
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe  
-70 -65 -60 -55  
Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp  
-50 -45 -40  
Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val  
-35 -30 -25  
Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp  
-20 -15 -10  
Thr Ala Val Thr Ser Gly Arg Gly  
-5 1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -68..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln Arg Phe Phe Gln

-65                      -60                      -55  
 Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln Ala Ala Leu Glu  
      -50                      -45                      -40  
 Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp Ala Gln Tyr Tyr  
      -35                      -30                      -25  
 Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn Tyr Cys Val Ala  
      -20                      -15                      -10                      -5  
 Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro Asn Asn Ser Thr  
                              1                               5                               10  
 Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu Lys Asn Tyr Ala  
              15                               20                               25  
 Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly  
              30                               35

## (2) INFORMATION FOR SEQ ID NO: 537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly Tyr Ala Gln Glu Asp  
      -60                      -55                      -50                      -45  
 Arg Glu Arg Met His Arg Asn Ile Val Ser Leu Ala Gln Asn Leu Leu  
              -40                               -35                               -30  
 Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp  
              -25                               -20                               -15  
 Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro  
              -10                               -5                               1  
 Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu Asn Ala Ala Trp Pro  
              5                               10                               15                               20

Arg

## (2) INFORMATION FOR SEQ ID NO: 538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq WSPLSTRSGGTHA/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
-30 -25 -20

Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys  
-15 -10 -5 1

Ser Ala Ser Met Arg Gln Pro Trp  
5

## (2) INFORMATION FOR SEQ ID NO: 539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq SILAQVLDQSARA/RL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu  
                     -50                    -45                    -40

Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala  
                     -35                    -30                    -25

Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu  
                     -20                    -15                    -10

Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro  
                     -5                    1                    5                    10

Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr  
                     15                    20                    25

Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu  
                     30                    35                    40

Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr Thr Val Arg  
                     45                    50                    55

## (2) INFORMATION FOR SEQ ID NO: 540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq GLVCAGLADMARPAE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu  
                     -60                    -55                    -50

Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr  
                     -45                    -40                    -35

Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met  
                     -30                    -25                    -20

Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala  
                     -15                    -10                    -5                    1

Glu Lys Leu Ser Thr Ala Gln Ser Xaa Val Leu Met Ala Thr Gly Phe  
                     5                    10                    15

Ile Trp Ser Arg Tyr Ser  
20

## (2) INFORMATION FOR SEQ ID NO: 541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq TGXLNMTLQRASA/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Ser Asn Tyr Ser Val Ser Leu Val Gly Pro Ala Pro Trp Gly Phe
-85 -80 -75

Arg Leu Gln Gly Gly Lys Asp Phe Asn Met Pro Leu Thr Ile Ser Ser
-70 -65 -60 -55

Leu Lys Asp Gly Gly Lys Ala Ala Gln Ala Asn Val Arg Ile Gly Asp
 -50 -45 -40

Val Val Leu Ser Ile Asp Gly Ile Asn Ala Gln Gly Met Thr His Leu
 -35 -30 -25

Glu Ala Gln Asn Lys Ile Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr
 -20 -15 -10

Leu Gln Arg Ala Ser Ala Ala Pro Lys Pro Glu Pro Val Pro Val Gln
-5 1 5 10

Lys Pro Thr Val Thr Ser Val Cys Ser Glu Thr Ser Gln Glu Leu Ala
 15 20 25

Glu Gly Gln Arg Arg Gly Ser Gln Gly Asp Ser Lys Gln Gln Asn
 30 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 542:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LLGLELSEAEAG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala  
-15 -10 -5  
Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser  
1 5 10  
Lys Glu Leu Gln Gln  
15

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq ALLCTLLLHFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ile Ile Pro Leu Leu Glu Ile Leu Ile Ile Val Leu Asn Glu  
-40 -35 -30 -25  
Val Leu Leu Phe Asp Val Asn Ser Val Tyr Lys Ala Leu Leu Cys Thr  
-20 -15 -10  
Leu Leu Leu His Phe Gln Asn Ile Arg Arg Phe Leu Ser Ser Gln Ser  
-5 1 5  
Pro Met Lys Ala Val Ser Leu Leu Xaa Phe His Gln Pro Asp Phe Asp

10

15

20

Tyr Ile  
25

## (2) INFORMATION FOR SEQ ID NO: 544:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LVFIIGLVGNLLA/LV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro Pro Ser Ala Thr Pro
 -50 -45 -40

Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His Ser Thr Ala Arg Ile
 -35 -30 -25

Val Met Pro Leu His Tyr Ser Leu Val Phe Ile Ile Gly Leu Val Gly
 -20 -15 -10 -5

Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn Arg Lys Lys Ile Asn
 1 5 10

Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe
 15 20 25

Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met Xaa Trp Ala Leu Thr
 30 35 40

Gly Glu Ser Glu Met Trp
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Pancreas

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -29..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7  
seq SMIGIGSLPSCWA/CW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser  
-25 -20 -15

Ser Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile  
-10 -5 1

Gln Gln Arg  
5



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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| <b>(51) International Patent Classification <sup>6</sup>:</b><br><b>C12N 15/12, C07K 14/47</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | <b>A3</b> | <b>(11) International Publication Number:</b> <b>WO 99/06548</b><br><b>(43) International Publication Date:</b> 11 February 1999 (11.02.99)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <b>(21) International Application Number:</b> PCT/IB98/01222<br><b>(22) International Filing Date:</b> 31 July 1998 (31.07.98)<br><b>(30) Priority Data:</b><br>08/905,135 1 August 1997 (01.08.97) US<br><b>(71) Applicant (for all designated States except US):</b> GENSET<br>[FR/FR]; 24, rue Royale, F-75008 Paris (FR).<br><b>(72) Inventors; and</b><br><b>(75) Inventors/Applicants (for US only):</b> DUMAS MILNE ED-<br>WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours,<br>F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter,<br>rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno<br>[FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval<br>(FR).<br><b>(74) Agents:</b> MARTIN, Jean-Jacques et al.; Cabinet Régimbeau,<br>26, Avenue Kléber, F-75116 Paris (FR). |           | <b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR,<br>BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE,<br>GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ,<br>LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW,<br>MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL,<br>TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO<br>patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian<br>patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European<br>patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR,<br>IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF,<br>CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).<br><br><b>Published</b><br><i>With international search report.</i><br><i>Before the expiration of the time limit for amending the claims</i><br><i>and to be republished in the event of the receipt of amendments.</i><br><br><b>(88) Date of publication of the international search report:</b><br>8 April 1999 (08.04.99) |
| <b>(54) Title:</b> 5'ESTs FOR NON TISSUE SPECIFIC SECRETED PROTEINS<br><br><b>(57) Abstract</b><br><br>The sequences of 5'ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5'ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5'ESTs. The 5'ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5'ESTs. The 5'ESTs may also be used to design expression vectors and secretion vectors.                                                                                                                                                                                                                                                            |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

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## INTERNATIONAL SEARCH REPORT

International Application No.

PCT/B 98/01222

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                         | Relevant to claim No. |
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

9 November 1998

Date of mailing of the international search report

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## INTERNATIONAL SEARCH REPORT

International Application No

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## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                                                             | Relevant to claim No. |
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|            | ---<br>-/--                                                                                                                                                                                                                                                                                                                                                    |                       |

# INTERNATIONAL SEARCH REPORT

International Application No

PC B 98/01222

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                      | Relevant to claim No. |
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| A          | <p>TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins"</p> <p>SCIENCE,<br/>vol. 261, 30 July 1993, pages 600-603,<br/>XP000673204</p> <p>---</p>           |                       |
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# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 98/01222

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-37 all partially (Invention 1. on continuation-sheet)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## 1. Claims: Invention 1: Claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:292, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

## 2. Claims: Inventions 2-254: Claims 1-37 all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-291, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 293, invention 3 is limited to Seq.ID:40 and 294,....., invention 254 is limited to Seq.ID:291 and 545).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

# INTERNATIONAL SEARCH REPORT

on patent family members

International Application No

IB 98/01222

| Patent document<br>cited in search report | Publication<br>date | Patent family<br>member(s) | Publication<br>date |
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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|
| (51) International Patent Classification 6 :<br>C12N 15/12, C07K 14/47                                                                                                                                                                                                                                                                                                                                                                                  |  | A3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | (11) International Publication Number:<br><b>WO 99/06548</b>     |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | (43) International Publication Date: 11 February 1999 (11.02.99) |
| (21) International Application Number: PCT/IB98/01222                                                                                                                                                                                                                                                                                                                                                                                                   |  | (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). |                                                                  |
| (22) International Filing Date: 31 July 1998 (31.07.98)                                                                                                                                                                                                                                                                                                                                                                                                 |  | <b>Published</b><br><i>With international search report.</i><br><i>With amended claims.</i>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                  |
| (30) Priority Data:<br>08/905,135 1 August 1997 (01.08.97) US                                                                                                                                                                                                                                                                                                                                                                                           |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |
| (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR).                                                                                                                                                                                                                                                                                                                                               |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |
| (72) Inventors; and<br>(75) Inventors/Applicants (for US only): DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR).                                                                                                                                        |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |
| (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Régimbeau, 26, Avenue Kléber, F-75116 Paris (FR).                                                                                                                                                                                                                                                                                                                                                     |  | (88) Date of publication of the international search report:<br>8 April 1999 (08.04.99)<br>Date of publication of the amended claims:<br>3 June 1999 (03.06.99)                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |
| (54) Title: 5'ESTs FOR NON TISSUE SPECIFIC SECRETED PROTEINS                                                                                                                                                                                                                                                                                                                                                                                            |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |
| (57) Abstract<br><p>The sequences of 5'ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5'ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5'ESTs. The 5'ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5'ESTs. The 5'ESTs may also be used to design expression vectors and secretion vectors.</p> |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |

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## AMENDED CLAIMS

[received by the International Bureau on 8 April 1999 (08.04.99);  
original claims 1-37 replaced by new claims 1-37 (5 pages)]

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 38-291 or comprising a sequence complementary thereto.
2. The nucleic acid of Claim 1, wherein said nucleic acid is recombinant.
- 5 3. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-291 or one of the sequences complementary thereto, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
- 10 4. A purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-291 or one of the sequences complementary thereto, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
- 15 5. The nucleic acid of Claim 4, wherein said nucleic acid is recombinant.
6. A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-291 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-291, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
- 20 7. The nucleic acid of Claim 6, wherein said nucleic acid is recombinant.
8. A purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-291, with the exception of a purified or isolated nucleic acid consisting of consecutive bases which are situated entirely in the sequences identified as Feature in the corresponding SEQ ID under key:other.
- 25 9. A purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-291 or having a sequence complementary thereto.
- 30 10. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 38-291 which encode a signal peptide.
11. A purified or isolated polypeptides comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-291.
12. A vector encoding a fusion protein comprising a polypeptide and a signal peptide, said vector comprising a first nucleic acid encoding a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-291 operably linked to a second nucleic acid encoding a polypeptide.
- 35 13. A method of directing the extracellular secretion of a polypeptide or the insertion of a polypeptide into the membrane comprising the steps of:

## AMENDED SHEET (ARTICLE 19)

obtaining a vector according to Claim 12; and

introducing said vector into a host cell such that said fusion protein is secreted into the extracellular environment of said host cell or inserted into the membrane of said host cell.

5 14. A method of importing a polypeptide into a cell comprising contacting said cell with a fusion protein comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-291 operably linked to said polypeptide.

15. A method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-291, comprising the steps of:

10 obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-291;

contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-291 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA;

identifying a cDNA which hybridizes to said detectable probe; and

15 isolating said cDNA which hybridizes to said probe.

16. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-291 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 15.

20 17. The cDNA of Claim 16 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-291.

18. A method of making a cDNA comprising one of the sequences of SEQ ID NOs: 38-291, comprising the steps of:

25 contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

hybridizing said first primer to said polyA tail;

reverse transcribing said mRNA to make a first cDNA strand;

making a second cDNA strand complementary to said first cDNA strand using least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NO

30 38-291; and

AMENDED SHEET (ARTICLE 19)